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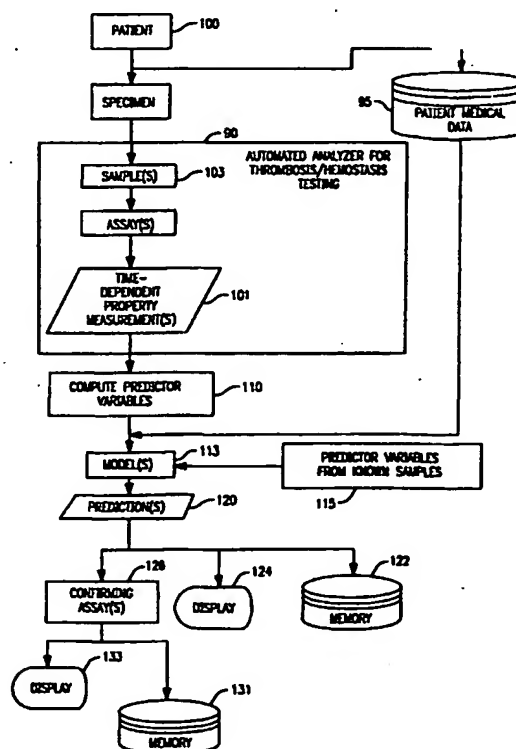
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(54) Title: A METHOD AND APPARATUS FOR PREDICTING THE PRESENCE OF HAEMOSTATIC DYSFUNCTION IN A PATIENT SAMPLE

(57) Abstract

A method is disclosed for predicting the presence of haemostatic dysfunction. At least one time-dependent measurement (101) on an unknown sample (103) is performed and a respective property of the sample (103) is measured over time so as to derive a time-dependent measurement profile. One or more predictor variables (110), including initial slope, are defined which sufficiently define the data of the time-dependent measurement profile. A model (113) is then derived that represents the relationship between an abnormality and a set of predictor variables (110). Subsequently, the model (113) is utilized to predict haemostatic dysfunction.



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**A Method and Apparatus for Predicting the Presence of
Haemostatic Dysfunction in a Patient Sample**

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BACKGROUND OF THE INVENTION

This application is a continuation-in-part of U.S. patent application 09/001,647, filed December 31, 1997, which is a continuation-in-part of U.S. patent application 08/859,773 to Givens et al. filed May 21, 1997, which is a continuation of U.S. patent application 08/477,839 to Givens et al. filed June 7, 1995, all of which are incorporated by reference. This application also relates to U.S. patent 5,646,046 to Fischer et al, the subject matter of which is incorporated herein by reference. This application is further related to the following publications, the subject matter of each also being incorporated herein by reference:

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Blood clots are the end product of a complex chain reaction where proteins form an enzyme cascade acting as a biologic amplification system. This system enables relatively few molecules of initiator
30 products to induce sequential activation of a series of inactive proteins, known as factors, culminating in the production of the fibrin clot. Mathematical models of the kinetics of the cascade's pathways have been previously proposed.

35 In [1], a dynamic model of the extrinsic

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coagulation cascade was described where data were collected for 20 samples using quick percent, activated partial thromboplastin time (APTT), thrombin time (TT), fibrinogen, factor(F) II, FV, FVII, FX, 5 anti-thrombin III (ATIII), and factor degradation product (FDP) assays. These data were used as input to the model and the predictive output compared to actual recovered prothrombin time (PT) screening assay results. The model accurately predicted the PT result 10 in only 11 of 20 cases. These coagulation cascade models demonstrate: (1) the complexity of the clot formation process, and (2) the difficulty in associating PT clot times alone with specific conditions.

15 Thrombosis and hemostasis testing is the in vitro study of the ability of blood to form clots and to break clots in vivo. Coagulation (hemostasis) assays began as manual methods where clot formation was observed in a test tube either by tilting the tube or 20 removing fibrin strands by a wire loop. The goal was to determine if a patient's blood sample would clot after certain materials were added. It was later determined that the amount of time from initiation of the reaction to the point of clot formation in vitro 25 is related to congenital disorders, acquired disorders, and therapeutic monitoring. In order to remove the inherent variability associated with the subjective endpoint determinations of manual techniques, instrumentation has been developed to 30 measure clot time, based on (1) electromechanical properties, (2) clot elasticity, (3) light scattering, (4) fibrin adhesion, and (5) impedance. For light scattering methods, data is gathered that represents the transmission of light through the specimen as a 35 function of time (an optical time-dependent

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measurement profile).

Two assays, the PT and APTT, are widely used to screen for abnormalities in the coagulation system, although several other screening assays can be used, 5 e.g. protein C, fibrinogen, protein S and/or thrombin time. If screening assays show an abnormal result, one or several additional tests are needed to isolate the exact source of the abnormality. The PT and APTT assays rely primarily upon measurement of time 10 required for clot time, although some variations of the PT also use the amplitude of the change in optical signal in estimating fibrinogen concentration.

Blood coagulation is affected by administration of drugs, in addition to the vast array of internal 15 factors and proteins that normally influence clot formation. For example, heparin is a widely-used therapeutic drug that is used to prevent thrombosis following surgery or under other conditions, or is used to combat existing thrombosis. The 20 administration of heparin is typically monitored using the APTT assay, which gives a prolonged clot time in the presence of heparin. Clot times for PT assays are affected to a much smaller degree. Since a number of other plasma abnormalities may also cause prolonged 25 APTT results, the ability to discriminate between these effectors from screening assay results may be clinically significant.

Using a sigmoidal curve fit to a profile, Baumann, et al [4] showed that a ratio of two 30 coefficients was unique for a select group of blood factor deficiencies when fibrinogen was artificially maintained by addition of exogenous fibrinogen to a fixed concentration, and that same ratio also correlates heparin to FII deficiency and FXa 35 deficiencies. However, the requirement for

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artificially fixed fibrinogen makes this approach inappropriate for analysis of clinical specimens. The present invention makes it possible to predict haemostatic dysfunction for clinical samples from a time-dependent measurement profile without artificial manipulation of samples.

The present invention was conceived of and developed for predicting haemostatic dysfunction in an unknown sample based on one or more time-dependent measurement profiles, such as optical time-dependent measurement profiles, where one or more predictor variables are provided which define characteristics of profile, and where in turn a model is derived that represents the relationship between the haemostatic dysfunction and the one or more predictor variables (so as to, in turn, utilize this model to predict the haemostatic dysfunction in the unknown sample). In addition, the present invention is directed to predicting the presence of Disseminated Intravascular Coagulation in a patient based on a time-dependent profile, such as an optical transmission profile, from a clotting assay run on the patient's blood or plasma sample.

25

SUMMARY OF THE INVENTION

The present invention is directed to a method and apparatus for predicting haemostatic dysfunction from at least one time-dependent measurement profile. The present invention is also directed to such a method and apparatus for predicting Disseminated Intravascular Coagulation (DIC). The method and apparatus include a) performing at least one assay on an unknown sample and measuring a respective property

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over time so as to derive a time-dependent measurement profile, b) defining one or more predictor variables (one of which is slope prior to clot formation) which sufficiently define the data of the time-dependent
5 profile, c) deriving a model that represents the relationship between a diagnostic output and the set of predictor variables, and d) utilizing the model to predict the existence of a haemosatic condition (e.g. DIC or septicemia) in the unknown sample relative to
10 the diagnostic output. In one embodiment, training data is provided by performing a plurality of assays on known samples, the model is a multilayer perceptron, the relationship between the diagnostic output and the one or more predictor variable is
15 determined by at least one algorithm, and the at least one algorithm is a back propagation learning algorithm. In a second embodiment of the present invention, the relationship between the diagnostic output and the at least one predictor variable is
20 derived by a set of statistical equations. Also in the present invention, a plurality of time-dependent measurement profiles are derived, which time-dependent measurement profiles can be optical time-dependent measurement profiles such as ones provided by a
25 automated analyzer for thrombosis and hemostasis, where a plurality of optical (e.g. optical transmission) measurements are taken over time, and where the plurality of optical measurements are normalized. The optical profiles can include one or
30 more of a PT profile, a fibrinogen profile, an APTT profile, a TT profile, a protein C profile, a protein S profile and a plurality of other assays associated with haemostatic dysfunction.

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BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a general neuron diagram relating to the embodiment of the present invention utilizing a neural network;

5 Figure 2 is a diagram of a multilayer perceptron for predicting congenital or acquired imbalances or therapeutic conditions, relating to the neural network embodiment of the present invention;

Figure 3 is an optical profile with first and
10 second derivatives of a normal clotting sample;

Figure 4 is an illustration of two learning curves;

Figure 5 is an illustration of an unstable learning curve;

15 Figure 6 is a graph showing a comparison of training and cross-validation learning curves;

Figure 7 is a graph showing a comparison of training error for training tolerances of 0.0 and 0.1;

Figure 8 is a ROC illustrating the effect of
20 decision boundary on classification;

Figure 9 is a Table comparing hidden layer size with prediction error;

Figure 10 is a receiver operator characteristic plot related to predicting an abnormality in relation
25 to Factor VIII;

Figure 11 is a graph demonstrating the ability to predict actual Factor VIII activity;

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Figure 12 is a receiver operator characteristic plot related to predicting an abnormality in relation to Factor X;

Figure 13 is a chart listing examples of
5 predictor variables for use in the present invention;

Figures 14 - 21 show ROC curves for neural networks trained to predict FII, FV, FVII, FVIII, FIX, FX, FXI, and FXII deficiencies from PT parameters alone, from APTT parameters alone, or from combined
10 APTT and PT parameters;

Figure 22 shows the constituency of the training and cross-validation sets with regard to each factor deficiency;

Figure 23 shows results of classification of
15 coagulation factor deficiencies as determined from area under ROC curves;

Figure 24 shows areas under ROC curves for three networks trained to classify factor deficiencies based on three different diagnostic cutoffs;

20 Figure 25 shows results from linear regressions comparing factor concentrations estimated using neural network with measured factor concentrations;

Figure 26 shows the correlation between neural network output and measured fibrinogen concentration
25 for cross-validation data set from neural networks trained to estimate fibrinogen concentration;

Figure 27 shows the correlation between neural network output and measured FX concentration for cross-validation data set from neural networks trained

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to estimate FX concentration;

Figure 28 shows SOM contour plots derived from APTT optical data for the six specimen categories;

Figure 29 shows contour plots for self-organizing 5 feature maps trained with PT data; and

Figure 30 shows the sensitivity, specificity, efficiency and predictive value of positive test (PPV) and the predictive value of negative test (NPV), based on either APTT or PT parameters.

10 Figure 31 is a chart illustrating steps of one embodiment of the invention;

Figure 32(A) and (B) illustrate transmittance waveforms on the APTT assay with (A) showing a normal appearance, and (B) a bi-phasic appearance, as derived
15 on the MDA-180, an automated Haemostasis-Thrombosis analyzer. The arrow signifies the point on the waveform where the clot time is recorded (in seconds) in relation to the X-axis. The dotted line indicates the light transmittance level at 25 seconds into the
20 reaction;

Figure 33 illustrates transmittance levels at 25 seconds in relation to diagnosis in the 54 patients with bi-phasic waveform abnormalities. The horizontal dotted line represents the normal transmittance level.
25 When more than one sequential analysis is available on a patient, the lowest transmittance level value is represented for that patient;

Figure 34 illustrates serial transmittance levels (upper panel) and waveforms (lower panel) on a patient
30 who developed DIC following sepsis and recovered;

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Figure 35 illustrates serial transmittance levels (upper panel) and waveforms (lower panel) on a patient who developed DIC following trauma and died;

Figure 36 illustrates ROC plots for the prediction of DIC for transmittance at 25 seconds (TR25), APTT clot time, and Slope1 (the slope up to initiation of clot formation);

Figures 37 and 38 show histograms for DIC, normal and abnormal/non-DIC populations for TR25 and slope 1 respectively;

Figures 39 and 41 show group distributions for slope 1 and TR25 respectively;

Figures 40 and 42 show partial subpopulations of the data shown in Figures 39 and 41;

Figure 43 is an optical transmission profile for an APTT assay; and

Figures 44 and 45 are optical transmission profiles for PT assays.

20

DESCRIPTION OF THE PREFERRED EMBODIMENTS

In the present invention, both a method and apparatus are provided for predicting the presence of the existence of haemostatic dysfunction in a patient sample. As can be seen in Figure 31, one or more time-dependent measurements (101) are performed on an unknown sample (103). The term "time-dependent measurement" is referred to herein to include

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measurements derived from assays (e.g. PT, APTT, fibrinogen, protein C, protein S, TT, ATIII, plasminogen and factor assays). The terms "unknown sample" and "clinical sample" refer to a sample, such as one from a medical patient (100), where haemostatic dysfunction associated with thrombosis/hemostasis is not known (or, if suspected, has not been confirmed).

In the present invention, a coagulation property is measured over time so as to derive a time-dependent measurement profile. In a preferred embodiment, the time-dependent measurement is an optical measurement for deriving an optical profile. For example, a PT profile, a fibrinogen profile, a TT profile, an APTT profile and/or variations thereof can be provided where, an unknown sample is analyzed for clot formation based on light transmittance over time through the unknown sample. In another preferred embodiment, two (or more) optical profiles are provided, such as both a PT profile and an APTT profile.

After the time-dependent measurement profiles are provided, a set of predictor variables are defined (110) which sufficiently define the data of the time-dependent profile. One or more predictor variables comprise the set. And, in one embodiment, three or more, and in a preferred embodiment, four or more predictor variables were found to desirably make up the set. It was found that the characteristics of the time-dependent measurement profile could best be defined by one or more predictor variables, including the minimum of the first derivative of the optical profile, the time index of this minimum, the minimum of the second derivative of the optical profile, the time index of this minimum, the maximum of the second

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derivative, the time index of this maximum, the overall change in transmittance during the time-dependent measurement, clotting time, slope of the optical profile prior to clot formation, and slope of
5 the optical profile after clot formation.

After defining the set of predictor variables, a model (113) is derived which represents the relationship between a congenital or acquired imbalance or therapeutic condition and the set of
10 predictor variables. This model can be derived from a neural network in one embodiment of the present invention. In another embodiment, the model is derived via a set of statistical equations.

Neural networks represent a branch of artificial
15 intelligence that can be used to learn and model complex, unknown systems given some known data (115) from which it can train. Among the features of neural networks that make them an attractive alternative for modeling complex systems are :

- 20 1. They can handle noisy data well and recognize patterns even when some of the input data are obscured or missing.
2. It is unnecessary to determine what factors are relevant a priori since the network will
25 determine during the training phase what data are relevant, assuming there are at least some meaningful parameters in the set.

Neural networks are formed from multiple layers of interconnected neurons like that shown in Figure 1.
30 Each neuron has one output and receives input $i_1 \dots i_n$ from multiple other neurons over connecting links, or

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synapses. Each synapse is associated with a synaptic weight, w_j . An adder Σ or linear combiner sums the products of the input signals and synaptic weights $i_j * w_j$. The linear combiner output sum_i and θ_i (a threshold which lowers or a bias which raises the output) are the input to the activation function $f()$. The synaptic weights are learned by adjusting their values through a learning algorithm.

After deriving the model (113), whether based on neural networks or statistical equations, the model is utilized to predict (120) the existence of a congenital or acquired imbalance or therapeutic condition in the unknown sample relative to the time-dependent measurement profile(s). As such, a congenital or acquired imbalance or therapeutic condition can be predicted. Conditions which can be predicted as being abnormal in the present invention can include, among others, a) factor deficiencies, e.g. fibrinogen, Factors II, V, VII, VIII, IX, X, XI and XII, as well as ATIII, plasminogen, protein C, protein S, etc., b) therapeutic conditions, e.g. heparin, coumadin, etc., and c) conditions such as lupus anticoagulant. In one embodiment of the present invention, the method is performed on an automated analyzer (90). The time-dependent measurement profile, such as an optical data profile, can be provided automatically by the automated analyzer, where the unknown sample is automatically removed by an automated probe from a sample container to a test well, one or more reagents are automatically added to the test well so as to initiate the reaction within the sample. A property over time is automatically optically monitored so as to derive the optical profile. The predicted congenital or therapeutic

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condition (120) can be automatically stored in a memory (122) of an automated analyzer and/or displayed (124) on the automated analyzer, such as on a computer monitor, or printed out on paper. As a further
5 feature of the invention, if the predicted congenital or acquired imbalance or therapeutic condition (128) is an abnormal condition, then one or more assays for confirming the existence of the abnormal condition are performed on the automated analyzer. In fact, in a
10 preferred embodiment, the one or more confirming assays are automatically ordered and performed on the analyzer once the predicted condition is determined, with the results of the one or more confirming assays being stored in a memory (131) of the automated
15 analyzer and/or displayed (133) on the analyzer.

EXAMPLE 1: Prediction of Heparin in Sample

This example shows a set of predictor variables
20 that adequately describe screening assay optical profiles, develops an optimal neural network design, and determines the predictive capabilities of an abnormal condition associated with
thrombosis/hemostasis (in this case for the detection
25 of heparin) with a substantial and well-quantified test data set.

SimplastinTM L, PlatelinTM L, calcium chloride solution (0.025 M), imidazole buffer were obtained from Organon Teknika Corporation, Durham, NC, 27712,
30 USA. All plasma specimens were collected in 3.2% or 3.8% sodium citrate in the ratio of one part

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anticoagulant to nine parts whole blood. The tubes were centrifuged at 2000 g for 30 minutes and then decanted into polypropylene tubes and stored at -80°C until evaluated. 757 specimens were prepared from 2005 samples. These specimens were tested by the following specific assays: FII, FV, FVII, FVIII, FIX, FX, FXI, FXII, heparin, fibrinogen, plasminogen, protein C, and AT-III. Samples represented normal patients, a variety of deficiencies, and therapeutic conditions.

10 Of the specimen population 216 were positive for heparin determined by a heparin concentration greater than 0.05 units/ml measured with a chromogenic assay specific for heparin. The remaining specimens, classified as heparin-negative, included normal
15 specimens, a variety of single or multiple factor deficiencies, and patients receiving other therapeutic drugs. Positive heparin samples ranged to 0.54 units/ml.

PT and APTT screening assays were performed on each specimen
20 five days. When clot-based coagulation assays are performed by an automated optically-based analyzer such as the MDA 180, data are collected over time that represents the normalized level of light transmission through a sample as a clot forms (the optical
25 profile). As the fibrin clot forms, the transmission of light is decreased. The optical profile was stored from each test.

The network configuration chosen, a multilayer perceptron (M
condition. A similar network was also employed for
30 PT-only variables and APTT-only variables. This specific MLP consists of three layers: the input layer, one hidden layer, and the output layer.

A normal optical profile is shown in Figure 3.
The set of predictor variables were chosen with the
35 intent of describing optical profiles as completely as

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possible with a minimum number of variables. They are summarized in Table 1 where t is time from initiation of reaction, T is normalized light transmission through the reaction mixture, and pv_{jk} is the k th predictor variable of assay j .

The predictor variables were scaled to values between 0 and 1, based on the range of values observed for each variable for assay type k

$$i_j = f\left(pv_{jk}, \left(pv_{j,n,k}\right)_{\min}, \left(pv_{j,n,k}\right)_{\max}\right).$$

The input variable set includes i_1, \dots, i_7 for both a PT assay and APTT assay for each specimen. For known output variable values, heparin samples with results of greater than 0.05 units/ml were considered positive and assigned a value of 1 while negative samples were assigned a value of 0.

As the ratio of training set sample to the number of weights samples taken from the same distribution as the training set. Thus, small samples sizes, then can lead to artificially high classification rates. This phenomenon is known as overtraining. In order to achieve a true accuracy rate of 80%, a guideline for the number of samples in the training set is approximately five times the number of weights in the network. For most of this work, a 14-6-1 network was used, leading to an upward bound on the sample size of $O(450)$. To monitor and evaluate the performance of the network and its ability to generalize, a cross-validation set is processed at the end of each training epoch. This cross-validation set is a randomly determined subset of the known test set that is excluded from the training set.

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Once the input predictor variables and output values were determined for all specimen optical profiles, the 757 sets of data were randomly distributed into two groups: 387 were used in the training set and 370 were used in the cross-validation set. These same two randomly determined sets were used throughout all the experiments.

All synaptic weights and threshold values were initialized at the beginning of each training session to small random numbers.

The error-correction learning rule is an iterative process used to update the synaptic weights by a method of gradient descent in which the network minimizes the error as pattern associations (known input-output pairs) in the training set are presented to the network. Each cycle through the training set is known as an epoch. The order or presentation of the pattern associations was the same for all epochs.

The learning algorithm consists of six steps which make up the forward pass and the backward pass. In the forward pass, the hidden layer neuron activations are first determined

$$h = F(iW1 + \theta_h)$$

25

where h is the vector of hidden-layer neurons, i the vector of input-layer neurons, $W1$ the weight matrix between the input and hidden layers, and $F()$ the activation function. A logistic function is used as the activation function

$$F(x) = \frac{1}{1 + e^{-x}}$$

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Then the output-layer neurons are computed

$$o = F(hW2 + \theta_0)$$

5

where o represents the output layer, h the hidden layer and $W2$ the matrix of synapses connecting the hidden layer and output layers. The backward pass begins with the computation of the output-layer error

10

$$e_o = (o - d)$$

where d is the desired output. If each element of e_o is less than some predefined training error tolerance vector TE_{tol} , then the weights are not updated during that pass and the process continues with the next pattern association. A training error tolerance of 0.1 was used in all experiments unless otherwise specified. Otherwise, the local gradient at the output layer is then computed:

$$g_o = \alpha(1 - o)e_o$$

Next, the hidden-layer local gradient is computed:

25

$$g_h = h(1 - h)W2g_o$$

Once the hidden layer error is calculated, the second layer of weights is adjusted

30

$$W2_m = W2_{m-1} + \Delta W2$$

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where

$$\Delta W2 = \eta h g_0 + \gamma \Delta W2_{m-1}$$

5

is the learning rate, γ is the momentum factor, and m is the learning iteration. The first layer of weights is adjusted in a similar manner

10

$$W1_m = W1_{m-1} + \Delta W1$$

where

$$\Delta W1 = \eta i e + \gamma \Delta W1_{m-1}.$$

15

The forward pass and backward pass are repeated for all of the pattern associations in the training set, referred to as an epoch, 1000 times. At the end of each epoch, the trained network is applied to the cross-validation set.

Several methods were employed to measure the performance of the network's training. Error, E , for each input set was defined as

25

$$E = \sqrt{\frac{1}{N} \sum_{q=1}^N (d_q - o_q)^2}$$

The learning curve is defined as the plot of E versus epoch. The percent classification φ , describes the percent of the total test set (training and cross-

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validation) that is correctly classified based on some defined decision boundary, β . Receiver-Operating Characteristic (ROC) plots have also been utilized to describe trained networks' ability to discriminate between the alternative possible outcome states. In these plots, measures of sensitivity and specificity are shown for a complete range of decision boundaries. The sensitivity, or true-positive fraction is defined as

10

$$\text{sensitivity} = \frac{\text{true positive}}{\text{true positive} + \text{false negative}}$$

and the false-positive fraction, or (1-specificity) is defined as

15

$$(1 - \text{specificity}) = \frac{\text{false positive}}{\text{false positive} + \text{true negative}}$$

These ROC plots represent a common tool for evaluating clinical laboratory test performance.

20

Using the test set described, experiments were performed to determine if the presence of heparin could be predicted with this method. First, experiments were conducted to determine optimal error-correction backpropagation learning parameters: (1) hidden layer size, (2) learning rate, and (3) momentum. Additional experiments were also conducted to compare the performance of networks based on PT and APTT assays alone with that of one combining the results of both, the effect of the training error tolerance, and the decision boundary selection.

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Figure 9 shows the effect of the hidden layer size on the training and cross validation error and the percent correct classification for the optimal decision boundary, defined as the decision boundary which yielded the lowest total number of false positives and false negatives from the total test set.

As the hidden layer size is increased, the error is decreased. However, the ability to generalize does not increase after a hidden layer size of 6. The most significant benefit in terms of both error and percentage correct classification is between 4 and 6.

A hidden layer size of 6 was used for the remainder of the experiments.

A series of experiments were conducted with $\eta = \{0.01, 0.1, 0.5, 0.9\}$ and $\gamma = \{0.0, 0.1, 0.5, 0.9\}$. Figure 4 shows the learning curves for two of the best combinations of parameters.

Figure 5 shows an example learning curve when the learning rate is so high it leads to oscillations and convergence to a higher E . In general, as $\eta \rightarrow 0$ the network converged to a lower E and as $\gamma \rightarrow 1$, the rate of convergence improved. As $\eta \rightarrow 1$, the value of E converged too increased and oscillations increased.

In addition, as $\eta \rightarrow 1$, $\gamma \rightarrow 1$ exacerbated the oscillations.

Figure 6 shows a comparison of the learning curve for the training set and cross-validation set for $\eta=0.5$ and $\gamma=0.1$. It is a primary concern when developing neural networks, and it has been previously shown that it is important to look not only at the error in the training set for each cycle, but also the

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cross-validation error.

Figure 7 shows the learning curve $\eta=0.5$ and $\gamma=0.1$ and a learning tolerance of 0.0 and 0.1. These results suggest that a small learning tends to smoothen the convergence of the learning process.

Figure 8 shows the ROC plot for networks trained with the predictor variables from each of the two screening assays with that of them combined. In the single assay cases, the hidden layer size was 3. While using the data from one assay does lead to some success, using the information from both assays makes a significant improvement in the ability of the network to correctly predict the presence of heparin.

This graph indicates that a 90% true positive proportion can be achieved with a false positive proportion of 15%. Using a single assay, a 60-70% true positive proportion can be achieved with a false positive proportion of approximately 15%.

20 EXAMPLE 2: Factor VIII

Similar tests were run as in Example 1. As can be seen in Figures 10 and 11, two training sessions were conducted for predicting a Factor VIII condition in an unknown sample. Figure 10 is a receiver operator characteristic plot related to predicting an abnormality in relation to Factor VIII. In Figure 10, everything below 30% activity was indicated as positive, and everything above 30% was indicated as negative. Cutoff values other than 30% could also be used. In this Example, the activity percentage has a known accuracy of approximately + or - 10%. In Figure 11, the actual percent activity was utilized as the output.

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EXAMPLE 3: Factor X

As can be seen in Figure 12, the method of the present invention was run similar to that as in Example 2, where here an abnormality in Factor X concentration was predicted from unknown samples. Everything below 30% activity was indicated as positive, and everything above 30% was indicated as negative. Cutoff values other than 30% could also be used.

The results of the cross-validation sample sets throughout the experiments indicate that the sample size was sufficient for the network to generalize. While the random distribution of the training and cross-validation sets were held constant throughout the experiments presented, other distributions have been used. These distributions, while all yielding different results, still lead to the same general conclusion.

Many alternatives for or additions to the set of predictor variables were explored. This included coefficients of a curve fitted to the data profile, pattern recognition, and clot time-based parameters. Low order functions tend to lose information due to their poor fit, and high order functions tend to lose information in their multiple close solutions. Clot-based parameters, such as clot time, slope in the section prior to the initiation of clot formation, and afterwards, are often available, but not always (because in some samples, the clot time is not detectable). The successful results observed indicate that the set of predictor variables used are effective for predicting congenital or acquired imbalances or therapeutic conditions.

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The optimization of the network learning algorithm's parameters made significant differences in its performance. In general, performance was best with low learning rates, high momentum rates, some
5 small training error tolerance, and a hidden layer size approximately half of the size of the input layer.

10 ADDITIONAL EXAMPLES:

Optical measurements for APTT and PT assays were performed on MDA 180 instruments at a wavelength of 580 nm. Plasma specimens (n= 200) included normal patients, patients with a variety of coagulation
15 factor deficiencies and patients undergoing heparin or other anticoagulant therapy. Duplicate APTT and PT screening assays were performed on each specimen with two MDA 180s using single lots of APTT and PT reagents. These specimens were also analyzed using
20 specific assays for FII, FV, FVII, FVIII, FIX, FX, FXI, FXII, heparin, fibrinogen, plasminogen, protein C and antithrombin-III.

Data Processing and Neural Networks

25 Optical profile data files were exported from the MDA 180s and processed off-line. A set of nine parameters was derived to describe the timing, rate and magnitude of coagulation events. These parameters were calculated for all APTT and PT tests. The
30 parameter set is modified slightly from that for Example 1. In this approach, the optical data for a PT or APTT assay was divided into three segments (a pre-coagulation segment, a coagulation segment and a

-26-

post-coagulation segment) using divisions based on the minimum and maximum value of the second derivative for changes in optical signal with respect to time. The parameters that were analyzed included: (1) the times at which the onset, midpoint and end of the coagulation phase occur (*tmin2*, *tmin1* and *tmax2*; respectively); (2) mean slopes for the pre-coagulation phase and the post-coagulation phase (*slope1* and *slope3*, respectively) and the slope at the mid-point of coagulation (*min1*, the coagulation "velocity" at reaction midpoint, which is analogous to *slope2*); (3) terms for coagulation "acceleration" and "deceleration" (*min2* and *max2*, respectively); and (4) the magnitude of signal change during coagulation (*delta*).

Three different sets of data parameters were used as input to the neural network: (1) the nine parameters from PT assays, (2) the nine parameters from APTT assays, and (3) the combined parameters from the APTT and PT assays. Each specimen was run in duplicate on two instruments, to give a total of approximately 800 parameter sets from the 200 specimens. The total number varied slightly because of missing data due to insufficient sample, mechanical failure or unspecified failures. The data parameter sets were divided into training and cross-validation sets randomly by specimen where all replicates for a given specimen were grouped either in the cross-validation set or training set. The same training and cross-validation sets were used throughout this study. The method for training and cross-validation of the back-propagation neural networks has been described in relation to Example 1. Each neural network was trained for 1000 epochs. Training parameters were learning

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rate, 0.01; momentum, 0.5; learning tolerance, 0.10; decay, 0.05; input layer size, 18 (or 9 for single assays); hidden layer size, 9 (or 5 for single assays); and output layer size, 1. Three types of 5 networks were trained. These included networks that classified specimens as deficient or non-deficient based on a single diagnostic cut-off, sets of networks that used diagnostic cut-offs at different levels of the same factor, and networks trained to estimate the 10 actual concentration of a specific factor.

Classification of Factor Deficiencies Based on a Single Diagnostic Cut-off Level

In the first set of tests, neural networks were 15 trained to classify plasma samples into two groups, positive (factor-deficient) and negative (non-deficient), and results were compared to classification based on the measured factor concentration for the specimens. In most testing, the diagnostic cut-off for 20 defining factor deficiencies was set as 30%; that is, specimens with a measured concentration of less than 30% of normal for a specific factor were defined as deficient and those with greater than 30% activity were defined as non-deficient. These diagnostic cut-off 25 levels were arbitrarily defined, but are based on clinical requirements and reagent sensitivity. The desired output from positive samples and negative samples were defined as '1' and '0', respectively; the actual output for each specimen was a floating point 30 value, a , where $0 \leq a \leq 1$. Figure 22 shows the constituency of the training and cross-validation sets with regard to each factor deficiency. Classification of specimens was evaluated at varying "decision boundaries" that divided the neural network outputs into

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positive and negative groups. This positive or negative classification was then compared to the desired output (the known classification) for each input data set. Results were plotted as nonparametric receiver-operating 5 characteristic (ROC) curves and the areas under the curves were computed along with their associated standard errors. ROC curves were also derived for APTT and PT clot time values for comparison. Data points on the ROC curves represent the proportion of true-positive 10 and false-positive classifications at various decision boundaries. Optimum results are obtained as the true-positive proportion approaches 1.0 and the false-positive proportion approaches 0.0 (upper-left corner of graph). The optimum global measure of the ROC curve is 15 an area of 1.0.

Classification of Factor Deficiencies at Multiple Diagnostic Cut-off Levels

A second set of networks was trained for FX 20 classification in a similar manner to the first set except that the diagnostic cut-off level was varied (10%, 30%, and 50%). FX was chosen for this experiment because the data set contained a greater number of positive samples at all cut-off levels than other 25 factors.

Estimation of Factor Concentration Using Neural Networks

A third set of networks were trained to approximate 30 actual specific factor activities (FII, FV, FVII, FVIII, FIX, FX, FXI and FXII) and fibrinogen levels from combined PT and APTT parameters from unknown samples. In these cases, the desired output of the training and cross-validation sets was the measured activity for a

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specific factor for each specimen and the actual output of the neural network was a predicted concentration for this specific factor activity. The coefficients of linear regressions using the desired outputs versus the 5 actual neural network outputs for the cross-validation set were used to describe the performance of these networks. The Pearson product moment correlation coefficient, r , was used to estimate the correlation between the two data sets.

10

Classification of Factor Deficiencies Based on a Single Diagnostic Cut-off Level

Neural networks were trained to classify samples as deficient (positive result) or non-deficient (negative 15 result) for individual plasma factors, using a value of 30% activity as the diagnostic cut-off to define deficiencies. Results were examined graphically using receiver-operating curves (ROC). These graphs plot the true-positive proportion (number of positives detected 20 divided by the total number of positives) versus the false-positive proportion (number of negative specimens incorrectly diagnosed as positive divided by the total number of negatives). An ROC curve is generated by determining true-positive and false-positive proportions 25 at different "decision boundaries" for the diagnostic test. For example, an ROC plot for diagnosis of FII deficiencies using PT clot time was generated by varying the decision boundary (value of PT clot time) used to differentiate between deficient and non-deficient 30 specimens. When a short clot time is used as the decision boundary, most deficient specimens can be identified but a significant proportion of non-deficient specimens may also be flagged (false-positives). When a long clot time is used as the decision boundary, the

-30-

proportion of false-positives decreases, but the number of true-positive specimens that are not diagnosed may also increase. Under ideal conditions, a decision boundary can be identified from an ROC curve that produces a very high proportion of true-positives and a very low proportion of false-positives. This condition corresponds to the upper left region of the ROC plot. Two related terms that are often applied to clinical diagnostic tests are "sensitivity" and "specificity".

10 Sensitivity refers to the ability to detect positive specimens and corresponds to the y-axis of the ROC plots. Specificity refers to the proportion of specimens diagnosed as negative which are correctly identified. The ROC x-axis equals (1-specificity).

15 Visual assessment of the ROC curves is one method used to evaluate the performance of the neural networks and compare them to the diagnostic power of PT and APTT clot times. Another method is to measure the diagnostic performance by using the area under the ROC curves. The

20 area under the ROC curve is equivalent to an estimate of the probability that a randomly chosen positive specimen will have a more positive result than a randomly chosen negative specimen. In the event that ROC curves overlap, the shape of the curves as well as the areas

25 beneath them becomes important. An ROC curve encompassing a smaller area may be preferable to an overlapping curve with greater area depending on the desired performance for a given diagnostic system.

Figures 14 - 21 show ROC curves for neural networks trained to predict FII, FV, FVII, FVIII, FIX, FX, FXI, and FXII deficiencies from PT parameters alone, from APTT parameters alone, or from combined APTT and PT parameters. ROC plots based on classification using APTT and PT clot times are included for comparison.

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Figure 23 shows the area under these curves and their associated standard errors.

Results for classification of FII deficiencies are shown in Figure 14. Best results were observed for 5 neural networks using APTT parameters alone or combined with PT parameters, with area under ROC curves greater than 0.99 in both cases (Figure 23). Classification based on PT or APTT clot times, or from neural networks using PT data alone resulted in less successful 10 classification and reduced area under curves.

Results from classification of FV deficiencies showed somewhat different characteristics (Figures 15 and 23). Best results were observed for classification from a neural network using APTT data parameters, based 15 on visual inspection and area under the ROC curve. Less successful classification were obtained from neural networks using PT data parameters alone or combined with APTT data, and from PT clot time, as judged from areas under ROC curves. Classification based on PT clot time 20 was qualitatively different from neural networks using PT data, however, and tended toward higher sensitivity rather than specificity. This type of pattern was observed for classification of several coagulation factors, especially factors VIII, X and XI. In 25 situations where overlapping ROC curves were obtained, consideration of the relative value of specificity and sensitivity, as well as the area under ROC curves, becomes important in comparing diagnostic results.

30 For several of these plasma factors, including FV, FVIII, FIX, FX, FXI and FXII (Figures 15, 17, 18, 19, 20 and 21), it appeared that it would be possible to achieve a moderately high true-positive proportion (> 0.6) while maintaining a low false-positive proportion

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(< 0.1) from neural networks using PT, APTT or combined parameters. This corresponds to a situation where a significant proportion of deficient specimens are not detected (moderate sensitivity), but those that are 5 detected are correctly classified as deficient for that specific factor (high specificity). In contrast, using PT or APTT clot times it was possible for most factors to adjust decision boundaries to identify most deficiencies (true-positive proportion approaching 1.0, 10 high sensitivity), but with a relatively high rate of false-positives (low specificity). This corresponds to a situation where most or all deficient specimens are detected, but where the specific factor deficiency is frequently not correctly identified. The first scenario 15 involving moderate or high true-positive rates with very low false positive rates may be preferable in the diagnostic scheme shown in Figure 13.

For factors II, V, IX and XII, it appeared that an appropriate choice of neural network gave best 20 diagnostic performance, as judged from the area under curves. For factors VIII, X and XI, neural networks were not visibly superior to diagnosis based on clot times when areas under ROC curves were the only consideration; however, neural networks for these factors did provide 25 better specificity. For one factor (FVII, Figure 16), neural network classification was less effective than for other factors, at least in this test system.

The performance of networks using data parameters from PT or APTT assays alone or in combination varied 30 for different factors. For factors VIII and XII, best performance (significantly greater area with no overlap) was observed when the combined sets of APTT-PT data parameters were used. For several other factors, use of a single parameter set provided results that were

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comparable to or better than the combined APTT and PT parameters. A network using only APTT data parameters (APTT NN) was equivalent (similar area) to a network using combined APTT-PT data (APTT-PT NN) for FII and FX; 5 and superior for FV (greater area and no overlap). Networks using only PT parameters provided results that were comparable (similar area) to the combined parameters for FV classification and better (greater area and insignificant overlap) for FIX classification.

10 The data for misclassified positive specimens were examined more closely. Misclassified positive specimens were clustered in several categories: 1) Specimens with "no clot" APTT or PT results (specimens with very prolonged or very weak coagulation reaction for which no
15 clot time can be reliably calculated); 2) specimens with multiple deficiencies or abnormalities; 3) specimens with borderline deficiencies (factor activity marginally lower than the diagnostic cut-off of 30%); and 4)
20 specimens with atypically steep slope during the pre-coagulation phase for APTT assays that were not characteristic of other specimens in the same classification (FX deficiencies were not detected for two specimens exhibiting this characteristic with FX activities of 26.8% and 16.8%, respectively).

25

Classification of Factor Deficiencies at Multiple Diagnostic Cut-off Levels

The ability of neural networks to classify FX-deficient specimens was tested at varying diagnostic
30 cut-offs. Areas under the ROC curves for cut-off levels of 10%, 30% and 50% FX activity are shown in Figure 24. Results indicate that progressively poorer classification (as expressed in smaller areas under ROC curves) was observed as higher cut-off levels were used.

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This was true for classification based on neural networks or PT clot times.

Neural Network Estimation of Factor Concentration

5 Neural networks were also trained to estimate actual protein concentrations (as opposed to a positive/negative classification at a defined cut-off) for FII, FV, FVII, FVIII, FIX, FX, FXI, FXII and fibrinogen. Linear correlation coefficients for the
10 estimated and measured concentrations are shown in Figure 25 for all experiments, and plots of the correlation data are shown in Figure 26 for fibrinogen and Figure 27 for FX. Correlation data between PT and APTT clot time and measured concentrations are also
15 shown in Figure 25 for comparison.

Example: Self-Organizing Feature Maps

Neural networks using self-organizing feature maps and learning vector quantization were used to analyze
20 optical data from clinical coagulation tests. Self-organizing feature maps using an unsupervised learning algorithm were trained with data from normal donors, patients with abnormal levels of coagulation proteins and patients undergoing anticoagulant therapy. Specimen
25 categories were distinguishable in these maps with varying levels of resolution. A supervised neural network method, learning vector quantization, was used to train maps to classify coagulation data. These networks showed sensitivity greater than 0.6 and
30 specificity greater than 0.85 for detection of several factor deficiencies and heparin.

An alternative approach to analyzing PT and APTT data with artificial neural networks (as set forth in

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Example 1) is by using self-organizing feature maps. Self-organizing feature maps contain layers of input and output neurons only and contain no hidden layers. Training is based on competitive learning where the 5 output neurons compete with one another to be activated and only one output neuron is activated for any given set of inputs. Output neurons become selectively tuned to certain input patterns, and data with similar features tend to be grouped together spatially. This 10 type of neural network may use either an unsupervised or supervised learning algorithm. When an unsupervised method is used, such as the self-organizing map (SOM) algorithm, unidentified input patterns are presented to the network during training and the output for each 15 input pattern is the coordinates of the winning neuron in the output layer, or map. When a supervised method is used, such as learning vector quantization (LVQ), input patterns are presented along with a known sample classification to the network during training and the 20 output is a unique predicted classification. The LVQ method is similar to SOM, except that the map is divided into classes, and the algorithm attempts to move outputs away from the boundaries between these classes.

MDA Simplastin L (PT reagent), MDA Platelin L (APTT 25 reagent) and other reagents were obtained from Organon Teknika Corporation, Durham, NC 27712, USA, unless otherwise indicated. Factor-deficient plasmas for factor assays were obtained from Organon Teknika and George King Bio-Medical Corporation, Overland Park, 30 Kansas 66210, USA. Additional factor-deficient plasmas were obtained from HRF, Raleigh, NC 27612, USA. Random samples, specimens from patients receiving heparin or oral anticoagulant therapy, and other specimens were obtained from Duke University Medical

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Center Coagulation Laboratory.

All testing was performed on MDA 180 coagulation analyzers (Organon Teknika). Optical measurements for PT and APTT assays were performed at a wavelength of 580 nm. Plasma specimens (n= 200) included normal patients, patients with a variety of deficiencies, and patients undergoing heparin or other anticoagulant therapy. Duplicate PT and APTT assays were performed on each specimen using two MDA 180s to give a total of approximately 800 parameter sets from the 200 specimens. The total number varied slightly because of missing data due to insufficient sample, mechanical failure or unspecified failures. These specimens were also tested to determine the concentration of coagulation factors (FII, FV, FVII, FVIII, FIX, FX, FXI, FXII) heparin, and fibrinogen. The diagnostic cut-off for defining factor deficiencies was set at 30%; that is, specimens with a measured concentration of less than 30% of normal for a specific factor were defined as deficient and those with greater than 30% activity were defined as non-deficient. Samples were defined as positive for heparin if the measured heparin concentration was greater than 0.05 IU/ml.

25 *Optical Data Processing*

Optical profile data files were exported from MDA 180s and processed off-line. A set of nine parameters was derived to describe the timing, rate and magnitude of coagulation events for PT and APTT tests, as described previously. In this approach, the optical data for a PT or APTT assay was divided into three segments (a pre-coagulation segment, a coagulation segment and a post-coagulation segment) using divisions based on the minimum and maximum value of the second

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derivative for changes in optical signal with respect to time. Parameters included: 1) the times at which the onset, midpoint and end of the coagulation phase occur; 2) mean slopes for the pre-coagulation phase and the post-coagulation phase and the slope at the mid-point of coagulation; 3) terms for coagulation "acceleration" and "deceleration"; and 4) the magnitude of signal change during coagulation.

10 Self-Organizing Map Algorithm

A self-organizing feature map neural network consists of input and output layers of neurons. The self-organizing map (SOM) algorithm transforms an input vector (a set of data parameters from PT or APTT optical data for a single test) to an individual output neuron whose location in the output layer, or map, corresponds to features of the input data. These features tend to be spatially correlated in the map. There are five steps in the SOM learning process:

- 20 1. Unique weight vectors $w_j(0)$, are randomly chosen.
2. A sample from the training set is selected.
3. The best-matching winning neuron $i(x)$ at time n , using the minimum-distance Euclidean criterion

25

is identified.

4. The weight vectors of all neurons are updated with the formula

30

where $\alpha(n)$ is the learning rate parameter, and $N_c(n)$

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5 is the neighborhood function centered around the winning neuron $i(x)$; both $\alpha(n)$ and $N_c(n)$ vary dynamically during training.

5. Steps 2 through 4 are repeated until the map reaches equilibrium.

10

The SOM tests were performed using the Self-Organizing Map Program Package (SOM_PAK) available from the Helsinki University of Technology, Laboratory of Computer Sciences. Two different sets of parameters
15 were used as input to the SOMs: (1) the nine parameters from a PT assay, and (2) the nine parameters from the APTT assay. All data sets (786) were used to train the SOMs. A 10x10 map was trained using a hexagonal neighborhood in two stages. In the first stage, the map
20 was trained for 1000 epochs (an epoch is one cycle through all data sets) with an initial learning rate parameter of 0.5 (decreasing linearly to zero during training) and a neighborhood radius of 10 (decreasing linearly to 1 during training). In the second stage,
25 the map was trained for 10000 epochs using a learning rate parameter of 0.1 and a radius of 3.

Learning Vector Quantization

Learning vector quantization (LVQ) is a supervised
30 learning algorithm often used to fine-tune self-organizing feature maps in order to use them in the role of a pattern classifier. The classification accuracy of the map is improved by pulling the weight vectors away from the decision surfaces that demarcate the class
35 borders in the topological map. There are several variations of the LVQ algorithm; the one used here is referred to as LVQ1. The learning process is similar to

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5 the SOM algorithm described above, except that known sample classifications are included when weight vectors are updated (step 4):

1. Initial weight vectors $w_j(0)$, are randomly chosen.
2. A sample from the training set with a known
10 classification is selected.
3. The best-matching winning neuron $i(x)$ at time n , using the minimum-distance Euclidean criterion

$$i(x) = \arg \min_j \{ \|x(n) - w_j(n)\| \}$$

15

is identified.

4. The weight vectors of all neurons are updated with the formula

$$20 \quad w_j(n+1) = \begin{cases} w_j(n) + \alpha(n)[x(n) - w_j(n)], & j=i, C_{w_j} = C_x \\ w_j(n) - \alpha(n)[x(n) - w_j(n)], & j=i, C_{w_j} \neq C_x \\ w_j(n), & j \neq i \end{cases}$$

where C_{w_j} is the class associated with the vector w_j and C_x is the class associated with the input vector x .

- 25 5. Steps 2 through 4 are repeated until the map reaches equilibrium.

The LVQ tests were performed using the Learning Vector Quantization Program Package (LVQ_PAK), also available from the Helsinki University of Technology,
30 Laboratory of Computer Sciences. The sets of parameters from the APTT assay or PT assays were used for the LVQ networks. The data parameter sets were divided evenly into training and cross-validation sets randomly by specimen, where all replicates for a given specimen were
35 grouped either in the cross-validation set or training set. The same training and cross-validation sets were

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5 used throughout this study. The LVQ networks were trained to classify plasma samples into two categories, positive (factor-deficient specimens or specimens from patients undergoing anticoagulant therapy) and negative (non-deficient or no anticoagulant therapy), and results
10 were compared to classification based on the measured factor concentration or therapeutic condition for the specimens. LVQ training was performed using 200 weight vectors, 10000 epochs, initial learning rate parameter of 0.5 (decreasing linearly to 0), and 7 neighbors used
15 in knn-classification.

LVQ networks were evaluated using sensitivity (the proportion of known positive specimens that were correctly classified as positive by the network), specificity (the proportion of known negative specimens
20 that were correctly classified as negative by the network), positive predictive value (PPV), negative predictive value (NPV) and efficiency. These terms are defined below, where TP, TN, FP and FN correspond to true positive, true negative, false positive and false
25 negative classifications, respectively.

$$\text{sensitivity} = \frac{TP}{TP + FN}$$

$$\text{specificity} = \frac{TN}{FP + TN}$$

30

$$\text{PPV} = \frac{TP}{TP + FP}$$

$$\text{NPV} = \frac{TN}{TN + FN}$$

35

$$\text{efficiency} = \frac{TN + TP}{TP + FP + FN + TN}$$

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5

Self-Organizing Map Algorithm

10 Self-organizing feature maps were trained using optical data parameters from either PT or APTT data for 200 specimens as input. Network output consisted of map coordinates for each specimen. Contour plots were constructed for six categories of known specimen
15 classifications: normal donors, specimens with heparin > 0.05 IU/ml, fibrinogen >600mg/dl, fibrinogen <200 mg/dl, patients receiving oral anticoagulants, and factor-deficient specimens (specimens with <30% of normal activity for FII, FV, FVII, FVIII, FIX, FX, FXI, or
20 FXII). These contour plots depict the distribution of specimens within a category according to their map coordinates.

Figure 28: Contour plots for populations of samples used in training a self-organizing feature map using the
25 unsupervised training method SOM based on data from APTT assays. Optical data parameters from 765 APTT assays were used to train this self-organizing feature map. The shaded areas represent the distribution of output neurons for specific specimen populations within the
30 feature map. Each contour line represents an incremental step of one test result located at a given set of map coordinates.

Figure 28 shows SOM contour plots derived from APTT optical data for the six specimen categories. Specimens
35 containing low fibrinogen and high fibrinogen were classified at opposite borders of the SOM with no overlap. Normal populations showed some overlapping

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5 with low fibrinogen, factor deficient and oral
anticoagulated categories. Overlap between normal
specimens and edges of the high and low fibrinogen
populations is expected, since some proportion of
healthy donors have fibrinogen levels that are lower or
10 higher than normal. Overlap between mapping of normal
specimens and factor-deficient plasmas is also not
surprising, since APTT tests are sensitive to some
factor-deficiencies (but not others), whereas PT assays
are sensitive to a separate subset of factor
15 deficiencies. The low fibrinogen category tended to
overlap the factor-deficient category, consistent with
our observation that many factor-deficient specimens
also had reduced fibrinogen levels. The heparin
category tended to overlap the high fibrinogen category,
20 again consistent with measured levels of fibrinogen for
these specimens. Little or no overlap was observed
between normal specimens and specimens containing
heparin. Specimens from patients receiving oral
anticoagulant therapy show significant overlap with both
25 normal and heparin populations. This is consistent with
known properties of APTT assays, which are sensitive to
heparin therapy but relatively insensitive to oral
anticoagulant therapy.

Figure 29: Contour plots for populations of samples
30 used in training a self-organizing feature map using the
unsupervised training method SOM based on optical data
from 765 PT assays. Experimental details are as
described in the Materials and Methods section and in
Figure 28.

35 Contour plots for self-organizing feature maps
trained with PT data are shown in Figure 29. Results
are similar to maps from APTT data in several respects:
(1) high and low fibrinogen were well resolved at

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- 5 opposite sides of the map; (2) normal specimens were localized in a region that overlapped low fibrinogen specimens slightly; (3) factor-deficient specimens were distributed between non-overlapping regions and regions that overlapped low fibrinogen and normal populations.
- 10 Overlap was consistent with measured fibrinogen for some specimens, and with poor sensitivity of PT reagents to some factor deficiencies in other cases; (4) oral anticoagulated specimens showed some overlap with both normal and heparin populations; and (5) the heparinized
- 15 population was distributed over a large portion of the map. Overlap between heparinized specimens and high fibrinogen populations was consistent with measured fibrinogen levels. The resolution of the heparin population is somewhat surprising, considering that PT
- 20 reagents are relatively insensitive to heparin.

These results indicate that self-organizing feature maps are capable of distinguishing differences in optical data parameters from APTT and PT assays even when no information regarding specimen diagnosis is

25 presented to the neural network. Resolution of specimen populations was variable, depending on reagent properties and sensitivities, and on whether specimens belonged to a given category uniquely or to multiple overlapping categories.

30

Learning Vector Quantization

- Eighteen LVQ networks were trained to predict the presence or absence of a specific factor deficiency or therapeutic condition from APTT or PT optical data.
- 35 Results for the cross-validation data are summarized in Figure 30. Previous studies concluded that back-propagation neural networks were capable of sensitivity > 0.6 while maintaining specificity > 0.9 for all factors

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5 except FVII using an appropriate choice of PT and APTT data separately or in combination. In this study, LVQ networks using APTT data gave sensitivity > 0.6 with specificity > 0.85 for factors II, X, XI, and XII, and heparin. LVQ networks using PT data were able to
10 achieve > 0.6 sensitivity while maintaining > 0.85 specificity for Factors II, X, and XI, and heparin (Figure 30). Results from LVQ networks showed less sensitivity for prediction of FVII deficiencies, consistent with results from back-propagation networks.
15 For FV, FVIII and FIX, sensitivity for predicting deficiencies from LVQ cross-validation sets was generally less (< 0.35) than for factors II, X, XI and XII.

20 Example: Haemostatic Dysfunction (e.g. Disseminated Intravascular Coagulation (DIC))

In a further embodiment of the invention, not only can a particular abnormality (Haemostatic Dysfunction)
25 be detected, but in addition the progression of the disease can be monitored in a single patient. Haemostatic Dysfunction, as used herein, is the activation of coagulation prior to initiation of clot formation, which results in a biphasic waveform.

30 Disseminated intravascular coagulation (DIC - a type of Haemostatic Dysfunction) prognosis has been hampered by the lack of an early, useful and rapidly available diagnostic marker. The invention has been found to be not only useful as an early diagnostic and
35 single monitoring marker of DIC, but in addition the quantifiable and standardizable changes also allow for prognostic applicability in clinical management.

Disseminated intravascular coagulation (DIC) is a

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5 secondary response to a pre-existing pathology whereby
the haemostatic response becomes perturbed and
disseminated as opposed to the focused events of normal
haemostasis. Despite improvements both in the intensive
care management of patients and in our basic knowledge
10 of haemostatic mechanisms in DIC, survival in this
patient group is still very discouraging. Fundamental
to the management of this complication is the
implementation of aggressive therapy directed at
forestalling or eradicating the primary pathology as the
15 source of the initiating stimulus. However, in
practical terms, the problem remains one of early
identification of DIC to facilitate immediate and
appropriate intervention. Although the technological
armory available to the clinical investigator has
20 expanded enormously, the pace of acute DIC precludes
most of the more specific tests and reliance is still
placed on traditional screening tests such as the
prothrombin (PT), activated partial thromboplastin time
(APTT) and platelet count. These tests lack specificity
25 on an individual basis and are only useful in DIC if
they lead on to further determinations of fibrinogen and
fibrin breakdown products/D-dimers. However, changes in
these parameters may not occur all at the same time and
as such, serial testing is often needed which inevitably
30 leads to a delay in diagnosis and clinically useful
intervention.

The normal sigmoidal appearance from an APTT
transmittance waveform (TW) changes to a "bi-phasic"
appearance in DIC patients. This represents a loss in
35 the plateau of a normal APTT-TW, with development of an
initial low gradient slope followed by a much steeper
slope (Figures 32a and b). In addition, this bi-phasic
pattern can be seen even when the APTT clotting time

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5 result is normal.

Freshly collected blood samples that required a PT or an APTT were analyzed prospectively over a two week working period. These were in 0.105M tri-sodium citrate in the ratio of 1 part anticoagulant to 9 parts whole blood and the platelet-poor plasma was analyzed on the MDA (Multichannel Discrete Analyzer) 180, an automated analyzer for performing clinical laboratory coagulation assays using an optical detection system (Organon Teknika Corporation, Durham, NC, USA). In addition, to deriving the clot times for both PT (normal 11.2-15s) using MDA Simplastin LS and APTT (normal 23-35s) using MDA Platelin LS with 0.025M calcium chloride (Organon Teknika Corporation, USA), an analysis of the TW for the APTT was performed on each occasion at a wavelength of 580nm. To quantitate the visual profile, the amount of light transmittance at 25 seconds was recorded. A normal waveform has a light transmittance of 100% which is represented on the analyzer and in Figure 32a without the decimal point as 10000. As such, a bi-phasic change will have a reduced light transmittance of less than 10000. Decreasing levels of light transmittance therefore correlates directly with increasing steepness of the bi-phasic slope. The recording of the light transmittance at 25 seconds also allows for standardization between patients and within the same patient with time. If the minimum level of light transmittance for each sample were to be used instead, this would be affected by variations in the clot time of the APTT and would therefore not be ideal for comparisons.

To ensure that no cases of DIC were overlooked, the following criteria was followed. If (a) an abnormal bi-phasic TW was encountered, or (b) a specific DIC screen

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5 was requested, or (c) if there was a prolongation in either the PT or APTT in the absence of obvious anticoagulant therapy, a full DIC screen was performed. This would further include the thrombin time (TT) (normal 10.5-15.5 seconds), fibrinogen (Fgn) (normal 1.5-10 3.8 g/l) and estimation of D-dimer levels (normal < 0.5 mg/l) on the Nyocard D-Dimer (Nycomed Pharma AS, Oslo, Norway). Platelet counts (Plt) (normal 150-400 $10^9/l$) performed on an EDTA sample at the same time were recorded. In addition, clinical details were fully 15 elucidated on any patient with a bi-phasic TW or coagulation abnormalities consistent with DIC.

The diagnosis of DIC was strictly defined in the context of both laboratory and clinical findings of at least 2 abnormalities in the screening tests (increased 20 PT, increased APTT, reduced Fgn, increased TT or reduced Plt) plus the finding of an elevated D-dimer level (>0.5 mg/l) in association with a primary condition recognized in the pathogenesis of DIC. Serial screening tests were also available on those patients to chart progression 25 and confirmation of the diagnosis of DIC as was direct clinical assessment and management. For statistical analysis, values for the sensitivity, specificity, positive and negative prediction of the APTT-TW for the diagnosis of DIC were calculated employing a two-by-two 30 table. 95% confidence intervals (CI) were calculated by the exact binomial method.

A total of 1,470 samples were analyzed. These were from 747 patients. 174 samples (11.9%) from 54 patients had the bi-phasic waveform change. 22 of these 54 35 patients had more than 3 sequential samples available for analysis. DIC was diagnosed in 41 patients with 30 of these requiring transfusion support with fresh frozen plasma, cryoprecipitate or platelets. The underlying

-48-

5 clinical disorders as shown in Table 1

Table 1: Clinical disorders predisposing patients to DIC.

	Disorder	No
10	Infections	17
	Trauma or recent major surgery	16
	Malignancy	2
	Hepatic Disease	1
	Obstetric Cause	1
	Miscellaneous Additional Causes •	4

• Includes hypoxia, acidosis, Lithium overdosage and graft rejection

15 40 of the 41 patients with DIC had the bi-phasic TW. The one false negative result (DIC without a bi-phasic TW) occurred in a patient with pre-eclampsia (PET) where the single sample available for analysis showed a prolonged PT of 21.0s, APTT of 44.0s and raised D-dimers 20 of 1.5mg/l. 5 other patients were identified in this study with PET and none had either DIC or a bi-phasic TW. Of the 14 patients with a bi-phasic TW which did not fulfil the criteria of DIC, all had some evidence of a coagulopathy with abnormalities in one or two of the 25 screening tests. These abnormal results fell short of the criterion for DIC as defined above. 4 of these 14 patients had chronic liver disease with prolonged PT and mild thrombocytopaenia. A further 2 patients had atrial fibrillation with isolated elevation of D-dimer levels 30 only. The remaining 8 patients were on the ICU with multiple organ dysfunction arising from trauma or suspected infection but without the classical laboratory changes of DIC. These patient profiles were described in the ICU as consistent with the "systemic inflammatory 35 response syndrome" (SIRS). Based on these figures, the bi-phasic TW has a 97.6% sensitivity for the diagnosis of DIC with a specificity of 98%. Use of an optical

-49-

5 transmittance waveform was found to be helpful in detecting the biphasic waveform.

Table 2: Performance of the transmittance waveform (TW) analysis in patients with and without DIC

10

	Biphasic TW	Normal TW	Total
DIC positive	40	1	41
DIC negative	14	692	706
Total	54	693	747

15

Sensitivity 97.6% (CI 85.6-99.9%), Specificity 98.0% (CI 96.6-98.9%), Positive predictive value 74.0% (CI 60.1-84.6%), Negative predictive value 99.9% (CI 99.1-99.9%)

The positive predictive value of the test was 74%, which increased with increasing steepness of the bi-phasic slope and decreasing levels of light transmittance (Table 2 and Figure 33). In the first two days of the study, there were 12 patients who had an abnormality in the clotting tests plus elevation of D-dimer levels. These were patients who were clinically recovering from DIC that occurred in the week preceding the study. This led to the impression that TW changes might correlate more closely with clinical events than the standard markers of DIC.

30

Table 3: Serial results in a patient with sepsis

Day	Time	PT (11.2-15s)	APTT (23-35s)	TT (10.5-15.5s)	Fgn (1.5-3.8 g/l)	D-Dimer (<0.5 mg/l)	Plt (150-400 x 10 ⁹ /l)	TW
1	0923	14.7	32.9	12.0	4.7	0.00	193	B*
1	2022	20.8*	38.6*	12.4	5.7	6.00*	61*	B*
2	0920	18.0*	33.0	13.0	5.2	2.00*	66*	N
3	1011	16.3*	24.8	13.2	4.7	0.00	64*	N

35

PT = Prothrombin time, APTT = Activated Partial Thromboplastin Time, TT = Thrombin Time, Fgn = Fibrinogen, Plt = Platelet count, TW = Transmittance Waveform

* Indicates abnormal changes. B = bi-phasic; N = normal

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5

The availability of more than 3 sequential samples in 22 patients allowed for further assessment. Table 3 illustrates one such example with serial test results from a patient with *E. coli* septicaemia.

- 10 The appearance of a bi-phasic TW preceded changes in the standard tests for the diagnosis of DIC. It was only later in the day that the PT, APTT, Plt and D-dimer levels became abnormal and fulfilled the diagnostic criteria of DIC. Treatment with intravenous antibiotics
15 led to clinical improvement by Day 2 with normalization of her TW in advance of the standard parameters of DIC. D-dimers and Plt were still respectively abnormal 24 and 48 hours later.

 This correlation between clinical events and TW
20 changes was seen in all the DIC patients where samples were available to chart the course of clinical events. As the TW changes were quantifiable and standardizable through recording of the transmittance level at 25 seconds, this analysis provided a handle in assessing
25 prognostic applicability. Figure 34 illustrates the results of a patient who initially presented with peritonitis following bowel perforation. This was further complicated by gram negative septicaemia post-operatively with initial worsening of DIC followed by a
30 gradual recovery after appropriate therapy. As DIC progressed initially, there was increasing steepness in the bi-phasic slope of the TW and a fall in the light transmittance level. A reversal of this heralded clinical recovery. Figure 35 illustrates the results of
35 a patient who sustained severe internal and external injuries following a jet-ski accident. Although initially stabilized with blood product support, his condition deteriorated with continuing blood loss and

-51-

5 development of fulminant DIC. The bi-phasic slope became increasingly steep with falls in transmittance level as the consequences of his injuries proved fatal.

As DIC can arise from a variety of primary
10 disorders, the clinical and laboratory manifestations can be extremely variable not only from patient to patient but also in the same patient with time. There is therefore, a need for systems that are not only robust in their diagnosis but simple and rapid to
15 perform. Although it has been shown that the bi-phasic TW appeared to be sensitive for Haemostatic Dysfunction (e.g. DIC) and was not seen in other selected patient groups with coagulation aberrations or influenced by either (i) pre-analytical variables, (ii) different
20 silica-based APTT reagents, (iii) the use of thrombin as the initiator of the coagulation reaction or (iv) treatment in the form of heparin or plasma expanders, the robustness of this assay for DIC could only be addressed through a prospective study. This study has
25 shown that the bi-phasic TW provides diagnostic accuracy in DIC with an overall sensitivity of 97.6% and specificity of 98%. In contrast, none of the standard parameters on an individual basis (i.e., PT, APTT, TT, Fgn, Plt, D-dimers) or even in combination, has ever
30 reached the degree of sensitivity or specificity. The ready availability of TW data from the MDA-180 would also fulfil the criteria of simplicity and rapidity unlike the measurements of thrombin-antithrombin complexes or other markers that are dependent on ELISA
35 technology. In addition, the advantages of TW analysis are that: (a) the bi-phasic TW change appears to be the single most useful correlate within an isolated sample for DIC and as such, reliance need no longer be placed

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5 on serial estimations of a battery of tests, and (b) the appearance or resolution of the bi-phasic TW can precede changes in the standard, traditional parameters monitored in DIC with strong, clear correlation to clinical events and outcome.

10 Although the bi-phasic TW was also seen in patients who did not have DIC *per se* as defined by the above criteria, the clinical conditions were associated with Haemostatic Dysfunction - namely activated coagulation prior to initiation of clot formation resulting in a
15 biphasic waveform (for example in chronic liver disease or in the very ill patients on the Intensive Care Unit who had multiple organ dysfunction). It appears that bi-phasic TW is sensitive to non-overt or compensated DIC and that a transmittance level of less than 90%
20 (Figure 33) or sequential falls in that level (Figure 35), reflects decompensation towards a more overt manifestation and potentially fulminant form of DIC. This line of explanation is supported by the observation of only a mild bi-phasic TW (transmittance level of
25 about 95%) in 2 patients with atrial fibrillation; a condition that is associated with mild coagulation activation and elevated D-dimer levels. As no follow-up samples were available on these 2 patients whose clinical details were otherwise unremarkable, their bi-
30 phasic TW could well have been transient. Nonetheless, these cases illustrate that the lower the level of light transmittance, the more likely the bi-phasic TW becomes predictive of Haemostatic Dysfunction, particularly DIC.

35 The observation of a normal TW in a patient with PET and DIC needs further exploration as the study did not selectively aim to examine any particular patient groups and only had a total of 6 patients with PET; the

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5 remaining 5 of which did not have DIC. One explanation
which would be supported by other findings in this study
is that the patient could have been recovering from PET
and DIC at the time of the sample. There may already
have been normalization in the bi-phasic TW in advance
10 of the other parameters which were still abnormal and
indicative of DIC. Another explanation is that the
disturbed haemostatic process in PET is more localized
and different from the DIC that arises from other
conditions. Such patients respond dramatically to
15 delivery of the fetus which suggests anatomical
localization of the pathological process to the placenta
despite standard laboratory clotting tests implying
systemic evidence of the condition.

Example:

20 Though analysis of the transmittance at a time of
25 seconds is helpful in predicting DIC, a second
embodiment of the invention has been found that greatly
improves sensitivity and specificity. It has been found
that looking at transmittance at a particular time can
25 result in detecting an artifact or other decrease in
transmittance at that point, even though the waveform is
not a bi-phasic waveform. For example, a temporary dip
in transmittance at 25 seconds would cause such a
patient sample to be flagged as bi-phasic, even if the
30 waveform was normal or at least not bi-phasic. Also, if
a patient sample had a particularly short clotting time,
then if clot formation begins e.g. prior to 25 seconds
(or whatever time is preselected), then the waveform
could be flagged as biphasic, even though the real
35 reason for decreased transmittance at 25 seconds is
because clot formation has already begun/occurred.

For this reason, it has been found that rather than
analysis of transmittance at a particular time, it is

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5 desirable to calculate the slope of the waveform prior
to initiation of clot formation. This calculation can
involve determination of clot time followed by
determination of waveform slope prior to clot time. In
an additional embodiment, the slope (not transmittance)
10 is determined prior to clot time or prior to a
preselected time period, whichever is less. As can be
seen in Figure 42, when transmittance is used for
determining e.g. DIC, there is poor specificity and
sensitivity. However, as can be seen in Figure 40, when
15 slope prior to initiation of clot formation is used,
specificity and sensitivity are greatly improved, and
are better than standard tests used in the diagnosis of
Haemostatic Dysfunction, such as DIC.

Additional testing was performed on three sets of
20 patients. The first set consisted of 91 APTT assays run
on samples from 51 different confirmed DIC patients.

The second set of data consisted of 110 APTT assays run
on samples from 81 different confirmed normal patients.

The third set of data included 37 APTT assays run on 22
25 abnormal, non-DIC samples. Fig. 36 illustrates ROC
plots for the prediction of DIC for three different
parameters derived from the APTT assay using the
combined data sets described: (1) transmittance at 25
seconds (TR25), (2) APTT clot time, and (3) slope 1 (the
30 slope up to initiation of clot formation). Slope 1
exhibited the best predictive power, followed by TR25.

It has also been shown that transmittance at 18 seconds
has predictive value, particularly when the APTT clot
time is less than 25 seconds. The "cutoffs" associated
35 with the highest efficiency for the three parameters are
listed in Table 4:

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Parameter	Cutoff
TR25	< 9700
Clot Time	> 35
Slope 1	< -0.0003

5

Table 4

It should be noted that these cutoffs have shifted with the addition of the third set, and would likely shift again, depending on the sample populations. Figures 37 and 38 show the histograms for the DIC, normal and abnormal/non-DIC populations for TR25 and slope 1 respectively. Tables 5 and 6 show the data for the histograms in Figures 37 and 38 respectively:

15

Bins	DIC	Normal	Abnormal/Non-DIC
-0.006	3	0	0
-0.005	2	0	0
-0.004	1	0	0
-0.003	10	0	0
-0.002	24	0	0
-0.001	33	0	0
-0.0005	12	0	0
-0.0002	5	5	2
-0.0001	1	37	13
More	0	68	22

5

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Table 5

<i>Bin</i>	DIC	Normal	Abnormal/Non-DIC
7000	34	1	0
8000	18	2	0
9000	26	6	1
9500	8	3	0
9600	3	2	1
9700	1	0	0
9800	1	3	0
9900	0	21	4
10000	0	62	30
More	0	10	1

Table 6

Figures 39 and 41 show the group distributions for Slope 1 and TR25 respectively; and Figures 40 and 42 show the group distributions for Slope 1 and TR25 respectively. Figures 40 and 42 show partial subpopulations of the data shown in Figures 39 and 41.

When the prediction of Haemostatic Dysfunction is performed on an automated or semi-automated analyzer, the detected bi-phasic waveform can be flagged. In this way, the operator of the machine, or an individual interpreting the test results (e.g. a doctor or other medical practitioner) can be alerted to the existence of the biphasic waveform and the possibility/probability of Haemostatic Dysfunction such as DIC. The flag can be displayed on a monitor or printed out. A slope of less than about -0.0003 or less than about -0.0005 is the preferred cutoff for indicating a bi-phasic waveform.

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5 An increasing steepness in slope prior to clot formation correlates to disease progression.

The above examples show that waveform analysis on the APTT assay can identify characteristic bi-phasic patterns in patients with haemostatic dysfunction. In
10 the majority of cases, this dysfunction could be labelled as DIC. This diagnostic waveform profile was seen in all APTT reagents tested, which were either silica or ellagic acid-based. It has also been
15 surprisingly found that a bi-phasic waveform can also be seen on PT assays with particular reagents, and that the bi-phasic waveform is likewise indicative of haemostatic dysfunction, primarily DIC.

Using samples that give bi-phasic APTT waveforms, the PT waveform profile was derived using PT reagents
20 (thromboplastin), namely Recombiplast™ (Ortho), Thromborel™ (Dade-Behring) and Innovin™ (Dade-Behring).

Both Recombiplast and Thromborel were particularly good at showing bi-phasic responses. Innovin was intermediate in its sensitivity. Using the
25 transmittance level at 10 seconds into the PT reaction as the quantitative index, Recombiplast and Thromborel objectively showed lower levels of light transmittance than Innovin. Thromborel can show a slight increase in initial light transmittance before the subsequent fall.
30 This may be, in part, related to the relative opaqueness of Thromborel.

Further studies were performed comparing APTT profiles using Platelin™ and PT waveform profiles using Recombiplast™. Consecutive samples over a four week
35 period from the intensive care unit were assessed. Visually, and on objective scores (comparing TL18 for APTT and TL10 for PT), the APTT profile was more sensitive to changes of haemostatic dysfunction and

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5 clinical progression than the PT profile. This relative
sensitivity can be seen in the APTT profile of Figure 43
(Platelin) compared to the PT profiles of Figure 44
(Recombiplast) and Figure 45 (Thromborel S).
Invariably, at smaller changes in light transmittance,
10 the APTT waveform detected abnormalities more easily than
the PT waveform. Nonetheless, in severe degrees of
haemostatic dysfunction, both bi-phasic profiles were
concordant.

It is to be understood that the invention described
15 and illustrated herein is to be taken as a preferred
example of the same, and that various changes in the
method and apparatus of the invention may be resorted
to, without departing from the spirit of the invention
or scope of the claims.

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5 WE CLAIM:

1. A method for predicting the presence of haemostatic dysfunction in a patient from at least one time-dependent measurement profile, comprising:

10 a) performing at least one time-dependent measurement on an unknown sample and measuring a respective property over time so as to derive a time-dependent measurement profile;

b) defining one or more predictor variables which
15 define, at least in part, the data of the time-dependent measurement profile, said one or more predictor variables including the slope of the time-dependent measurement profile prior to clot formation;

c) deriving a model that represents the
20 relationship between the haemostatic dysfunction and the one or more predictor variables; and

d) utilizing the model of step c) to predict the existence of haemostatic dysfunction in the patient.

2. A method according to claim 1, wherein said at
25 least one time-dependent measurement profile is at least one optical profile.

3. A method according to claim 3, wherein said at least one optical profile is provided by an automated analyzer for thrombosis and hemostasis testing.

30 4. A method according to claim 2, wherein a plurality of optical measurements at one or more wavelengths are taken over time so as to derive said at least one optical profile, said optical measurements corresponding to changes in light transmission through
35 the patient sample.

5. A method according to claim 2, wherein a plurality of optical measurements are taken over time so

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5 as to derive said at least one optical profile, and wherein said plurality of optical measurements are each normalized to a first optical measurement.

6. A method according to claim 3, wherein in step a) said at least one optical profile is provided
10 automatically by said analyzer, whereby said unknown sample is automatically removed by an automated probe from a sample container to a test well, one or more reagents are automatically added to said test well so as to initiate said property changes within said sample,
15 and the development of said property over time is automatically optically monitored so as to derive said optical data profile.

7. A method according to claim 6, wherein after step d), a predicted congenital or acquired imbalance or
20 therapeutic condition is automatically stored in a memory of said automated analyzer and/or displayed on said automated analyzer.

8. A method according to claim 6, wherein in step d), one or more assays for confirming the existence of
25 said congenital or acquired imbalance or therapeutic condition is automatically performed.

9. A method according to claim 8, wherein said one or more confirming assays are automatically ordered and performed on said analyzer, with results of said one or
30 more assays being stored in a memory of said automated analyzer and/or displayed on said analyzer.

10. A method according to claim 1, further comprising:
before step a), providing a set of data from known
35 samples, which data is used in step c) for deriving said model.

11. A method according to claim 10, wherein said

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5 data from known samples is provided by performing a plurality of assays on said known samples.

12. A method according to claim 1, wherein in step a), a plurality of time-dependent measurement profiles are derived for use in step b)..

10 13. A method according to claim 12, wherein said plurality of time dependent measurement profiles includes at least two profiles from assays initiated with PT reagents, APTT reagents, fibrinogen reagents and TT reagents.

15 14. A method according to claim 1, wherein said unknown sample is a sample from a medical patient, and wherein in step d), both said model and additional patient medical data are utilized for predicting the existence of said congenital or acquired imbalance or
20 therapeutic condition.

15. A method according to claim 14, wherein said additional patient medical data includes one or more of Fibrinogen, D-dimer or platelet count information.

16. A method according to claim 1, wherein in step
25 (d), the prediction of haemostatic dysfunction is performed a plurality of times so as to monitor disease progression or regression in the patient.

17. A method according to claim 1, wherein the prediction of haemostatic dysfunction is a prediction of
30 Disseminated Intravascular Coagulation.

18. A method according to claim 17, wherein said prediction of Disseminated Intravascular Coagulation is correct in at least 75% of predicted cases.

19. A method according to claim 1, wherein said
35 time-dependent measurement profile is an optical transmission through a sample during an APTT assay.

20. A method according to claim 1, wherein said

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5 time-dependent measurement profile is an optical transmission through a sample during a PT assay.

21. A method according to claim 1, wherein in step (b), the slope of the time-dependent measurement profile is taken from end of blank time up to immediately before
10 the initiation of clot formation or a predetermined time period.

22. A method according to claim 1, wherein said time-dependent measurement profile is an optical transmission profile and said one or more parameters
15 includes minimum transmittance and/or clot time.

23. A method according to claim 1, wherein said predicted haemostatic dysfunction is due to one or more conditions associated with disseminated intravascular coagulation, including trauma, malignancy, surgery,
20 aortic aneurysm rupture, and systemic inflammatory response syndrome.

24. A method according to claim 1, wherein said prediction of the existence of haemostatic dysfunction includes flagging the existence or likelihood of the
25 haemostatic dysfunction.

25. A method according to claim 1, wherein the only predictor variable is said slope of the time-dependent measurement profile prior to clot formation.

26. A method according to claim 1, wherein the
30 predictor variable of slope of the time-dependent measurement profile prior to clot formation is a slope which is less than about -0.0003.

27. A method according to claim 26, wherein said slope less than -0.0003 corresponds to activation of
35 coagulation prior to initiation of clot formation.

28. A method according to claim 1, wherein the predicted haemostatic dysfunction is due to one or more

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5 of infection, trauma, major surgery, malignancy, hepatic disease, pregnancy and/or child birth, hypoxia, acidosis, lithium overdose, and graft rejection.

29. A method according to claim 24, wherein method steps (a) to (d) are performed on an automated or semi-
10 automated analyzer, and said flagging is an alert to an individual operating said analyzer or an individual reading or evaluating the results of a test run on said analyzer, that there is a possibility or probability of haemostatic dysfunction of a patient whose test sample
15 has been run on the analyzer and flagged.

30. A method according to claim 29, wherein said alert is an alert on a paper printout or on a monitor.

31. A method according to claim 27, wherein a slope of less than -0.0003 causes flagging of the patient
20 sample, and wherein an increase in steepness of the slope from test to test corresponds to disease progression.

32. A method according to claim 1, wherein said patient sample is whole blood or a portion thereof.

25 33. A method according to claim 32, wherein said patient sample is a plasma sample.

34. A method according to claim 1, where said prediction of the existence of haemostatic dysfunction in the patient has a specificity and sensitivity greater
30 than other tests used in diagnosing haemostatic dysfunction.

35. A method according to claim 1, wherein said haemostatic dysfunction is disseminated intravascular coagulation, and wherein said prediction of disseminated
35 intravascular coagulation in the patient has a specificity and sensitivity greater than other tests performed for diagnosing disseminated intravascular

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5 coagulation.

36. A method according to claim 35, wherein said other tests are one or more of platelet count, determination of D-dimer level, and determination of fibrinogen level.

10 37. A method according to claim 1, wherein said haemostatic dysfunction predicted is disseminated intravascular coagulation, and wherein said method further comprises running platelet count, D-dimer level and/or fibrinogen level assays.

15 38. A method according to claim 1, wherein said slope is determined from blank time to initiation of clot formation or from blank time to a predetermined time period less than the time of initiation of clot formation, whichever is less.

20 39. A method according to claim 1, wherein the predictor variable of slope of the time-dependent measurement profile prior to clot formation is a slope less than about -0.0005.

40. A method according to claim 1, wherein said one
25 or more predictor variables are a plurality of predictor variable further comprising one or more of a minimum of the first derivative of the profile, a time index of the minimum of the first derivative, a minimum of the second derivative of the profile, a time index of the minimum
30 of the second derivative, a time index of the maximum of the second derivative, an overall change in the coagulation parameter during the time-dependent measurement on the unknown sample, a clotting time, a slope of the profile prior to clot formation, and a
35 slope of the profile after clot formation.

41. A method for predicting the presence of disseminated intravascular coagulation in a patient from a time-dependent measurement profile, comprising:

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- 5 a) performing a time-dependent measurement on
 an unknown sample and measuring a
 respective property over time so as to
 derive a time-dependent measurement
 profile;
- 10 b) computing the slope of the time-dependent
 measurement profile up to the initiation
 of clot formation or up to a predetermined
 time period less than the time of the
 initiation of clot formation, whichever is
15 less;
- c) computing a threshold for the parameter in
 c) from known positive and known negative
 samples which sufficiently separates
 positive and negative samples; and
- 20 d) utilizing the threshold in step c) to
 predict the existence of disseminated
 intravascular coagulation in the patient.

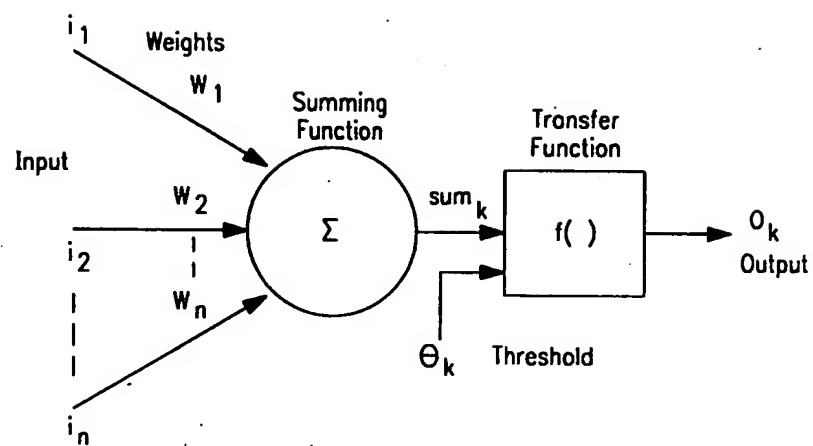


FIG. 1

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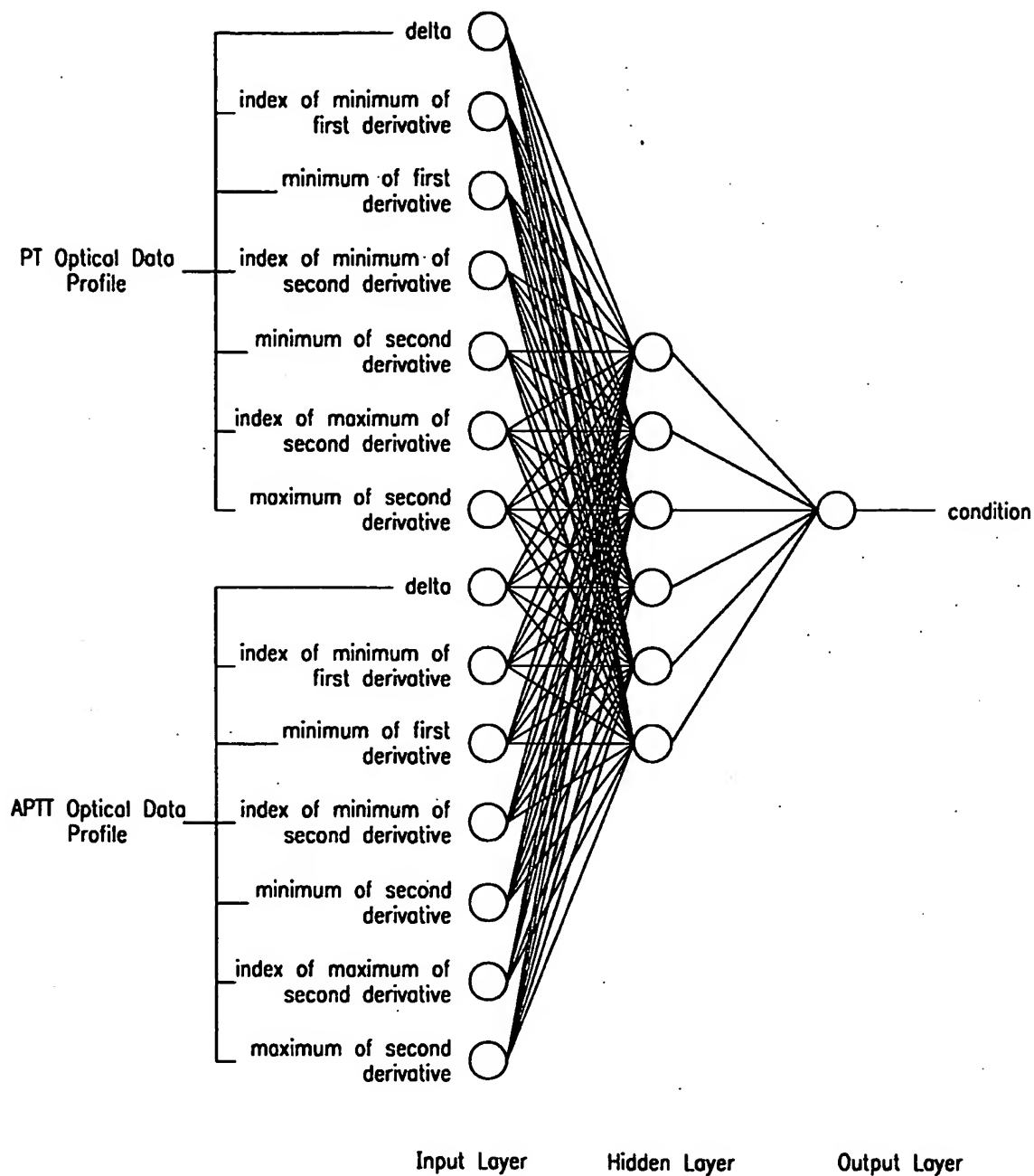


FIG. 2

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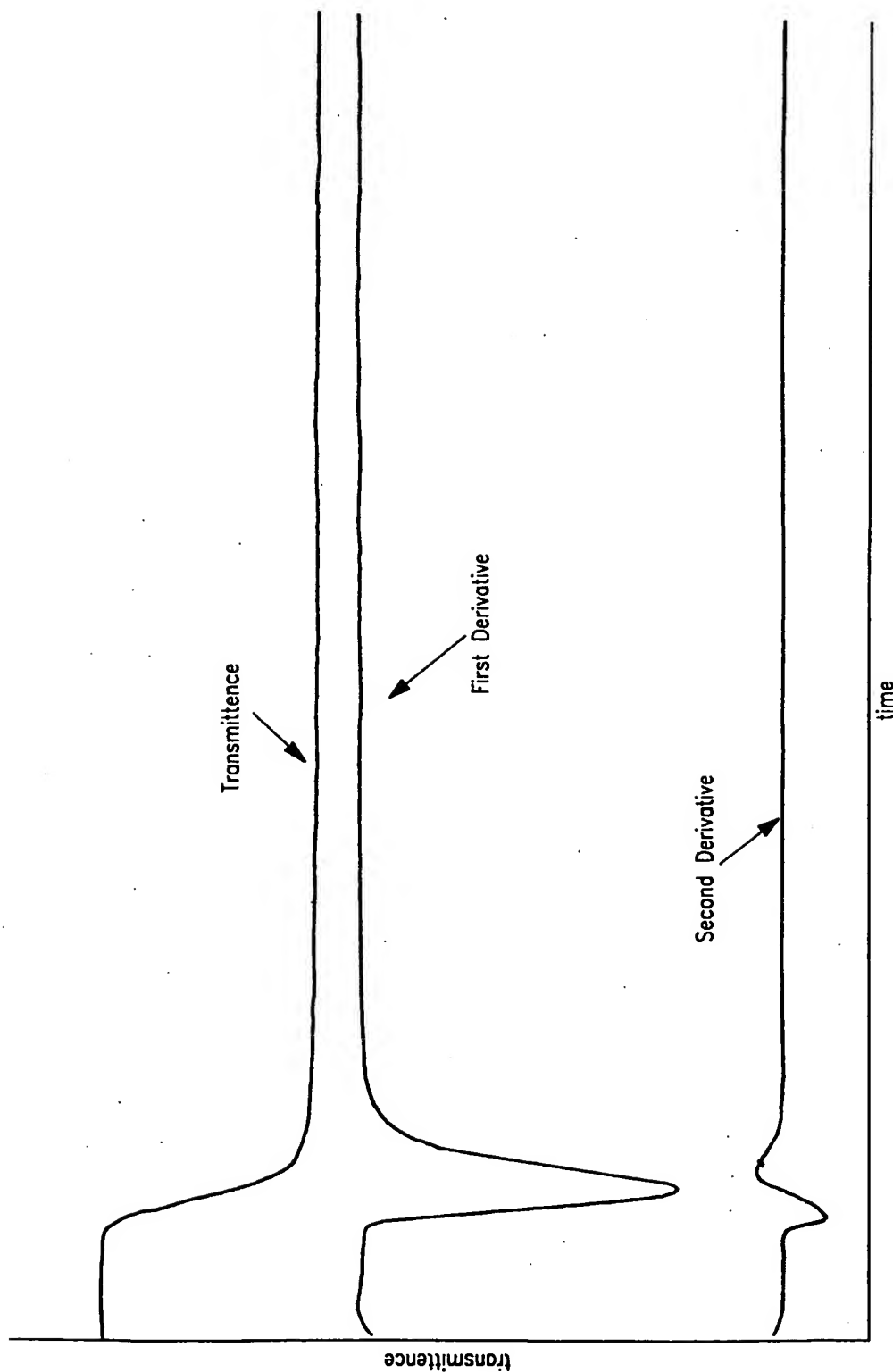


FIG. 3

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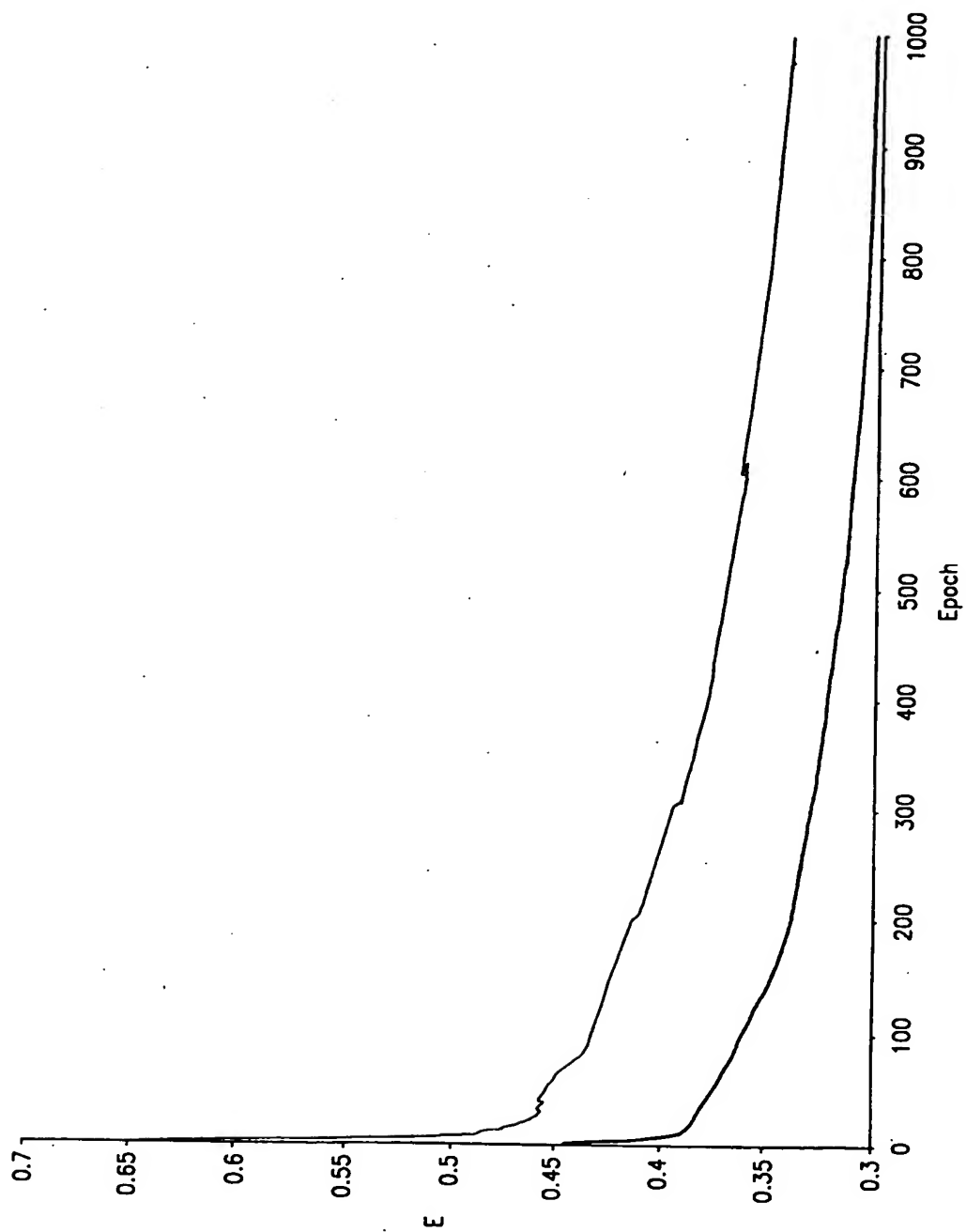
 $\eta=0.01, \alpha=0.9$ $\eta=0.5, \alpha=0.1$

FIG. 4

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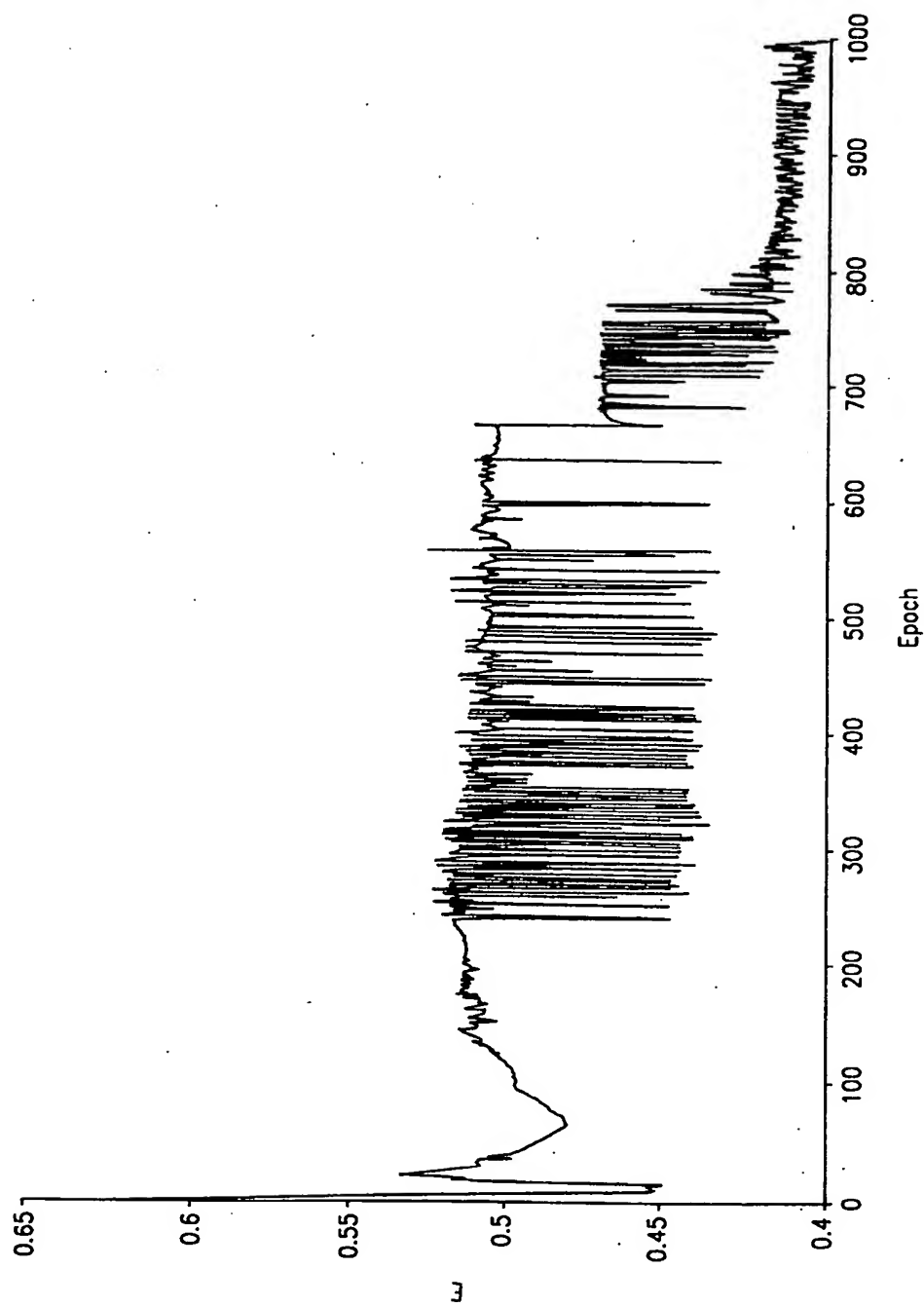
 $\eta=0.9, \alpha=0.1$

FIG. 5

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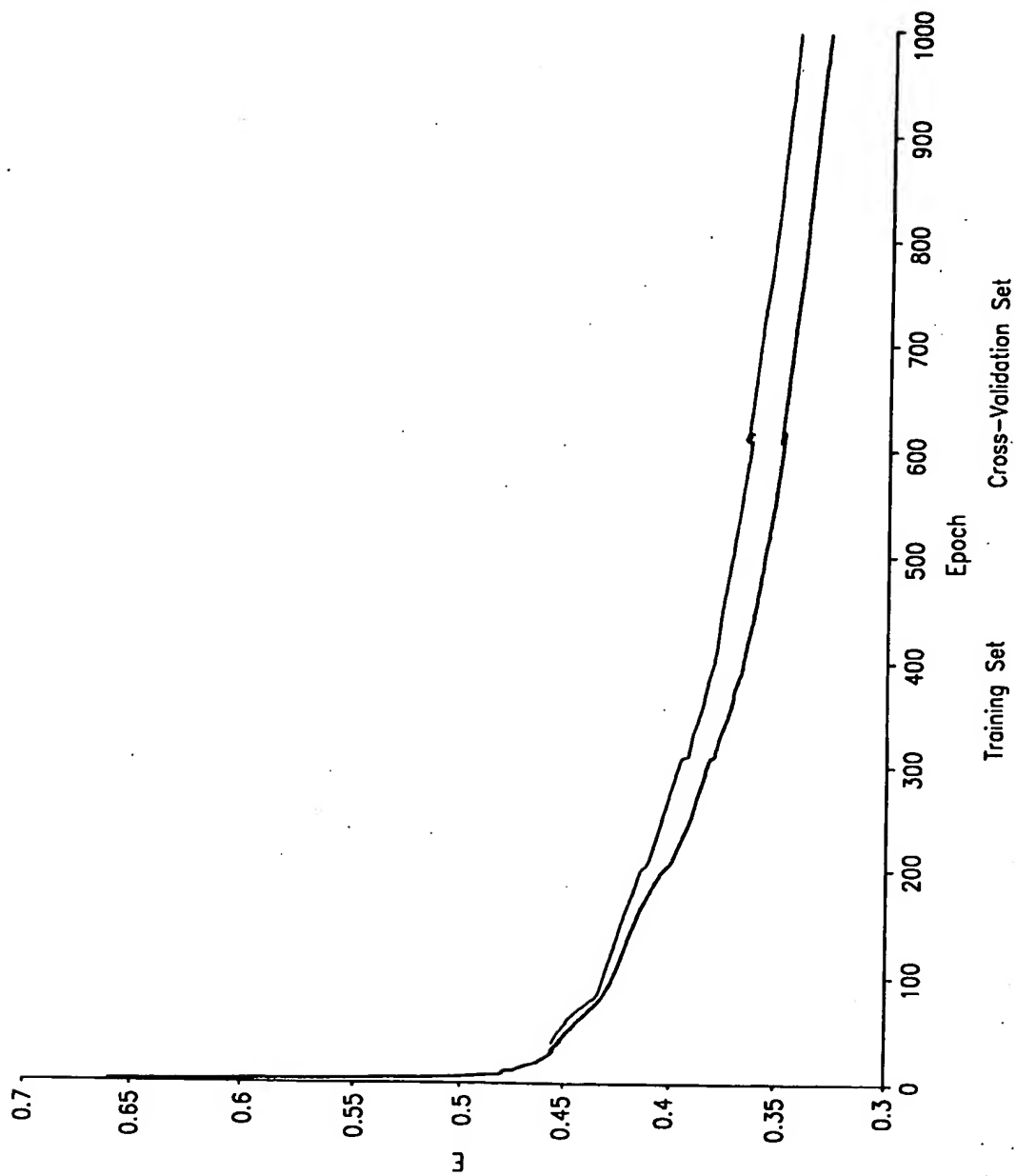


FIG. 6

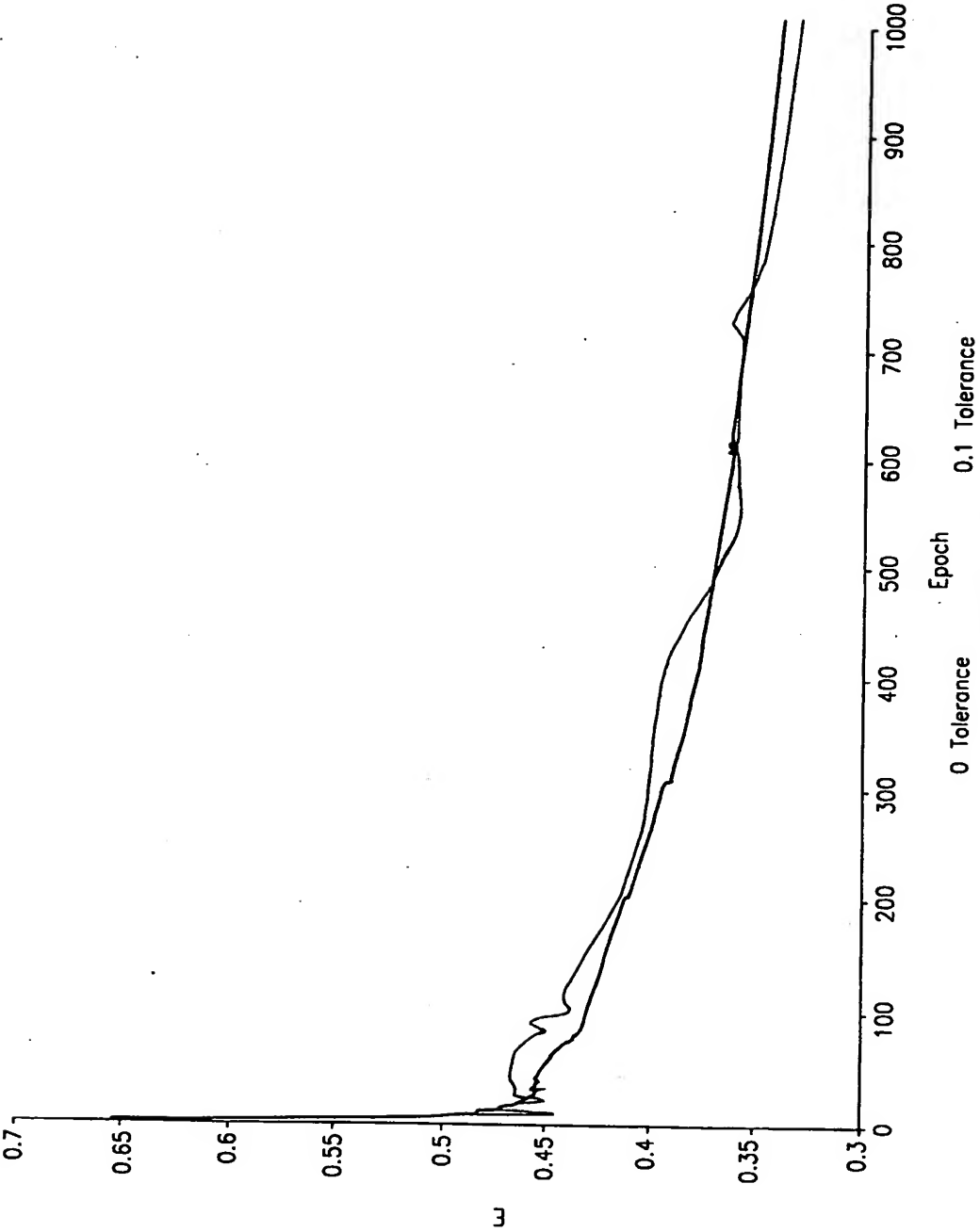


FIG. 7

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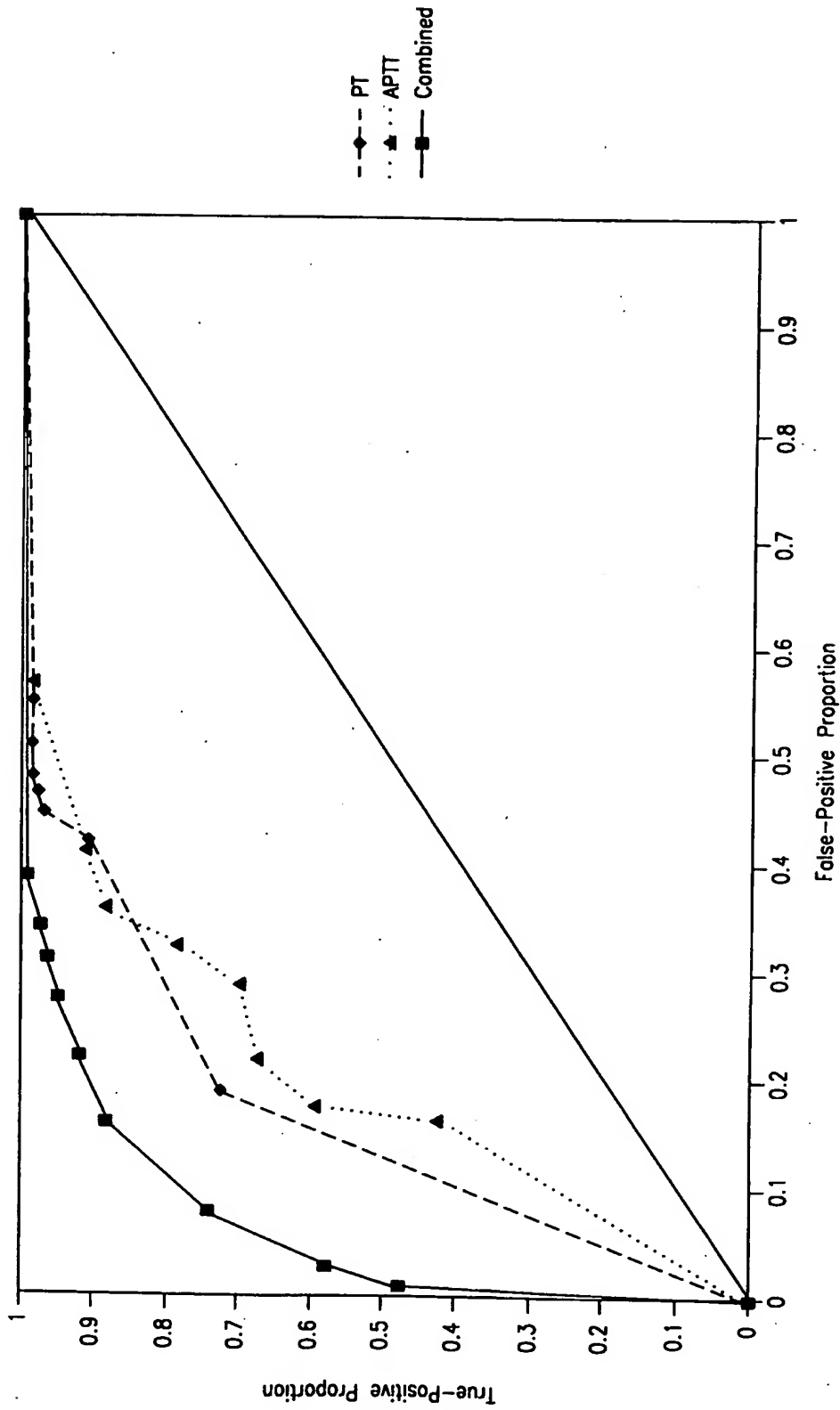


FIG. 8

Hidden Layer Size	Error		φ_{ODB}
	E_{tr}	E_{DV}	
2	0.384	0.376	0.848
4	0.386	0.354	0.835
6	0.341	0.328	0.875
8	0.358	0.327	0.857
10	0.346	0.325	0.856
12	0.347	0.322	0.855

FIG. 9

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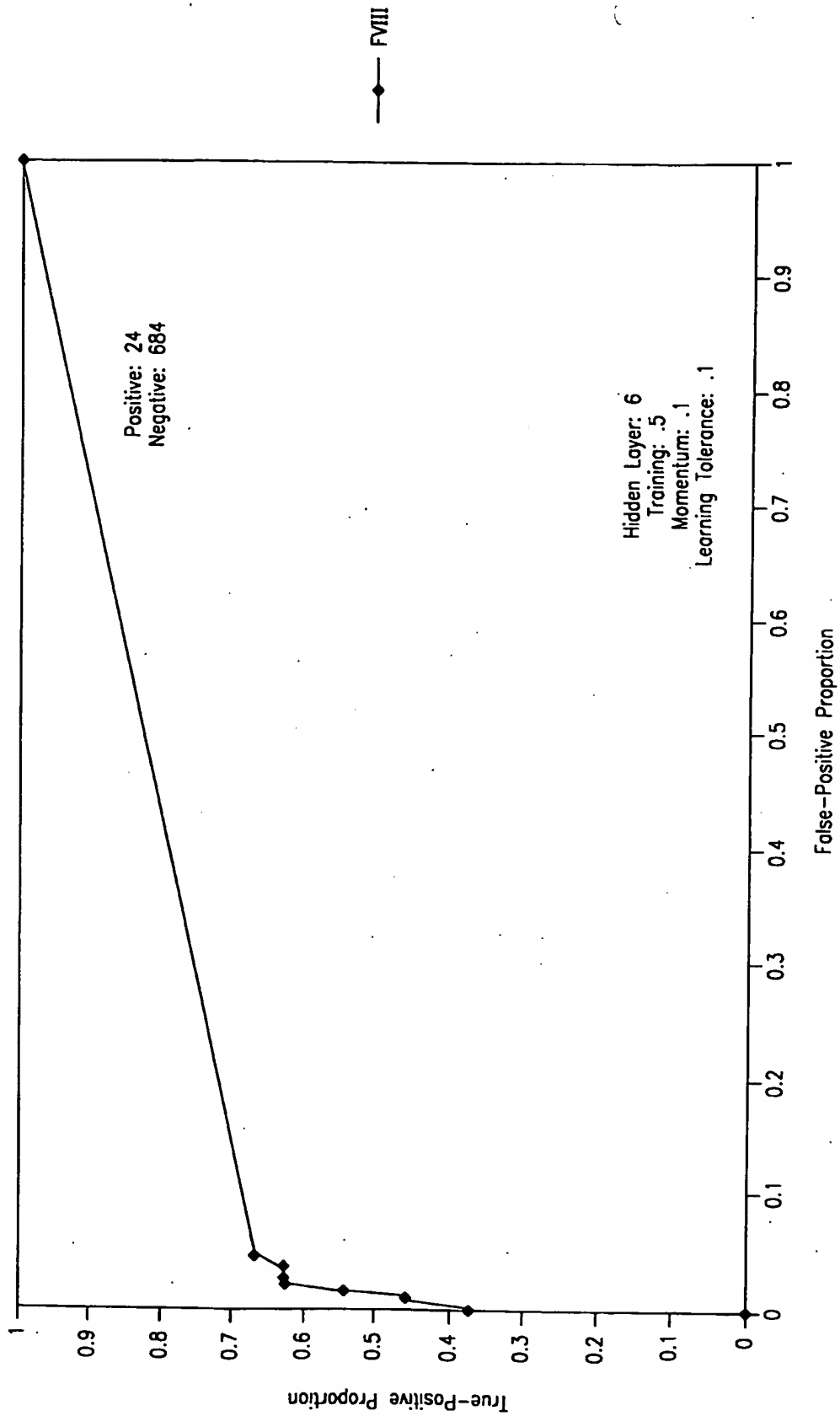


FIG. 10

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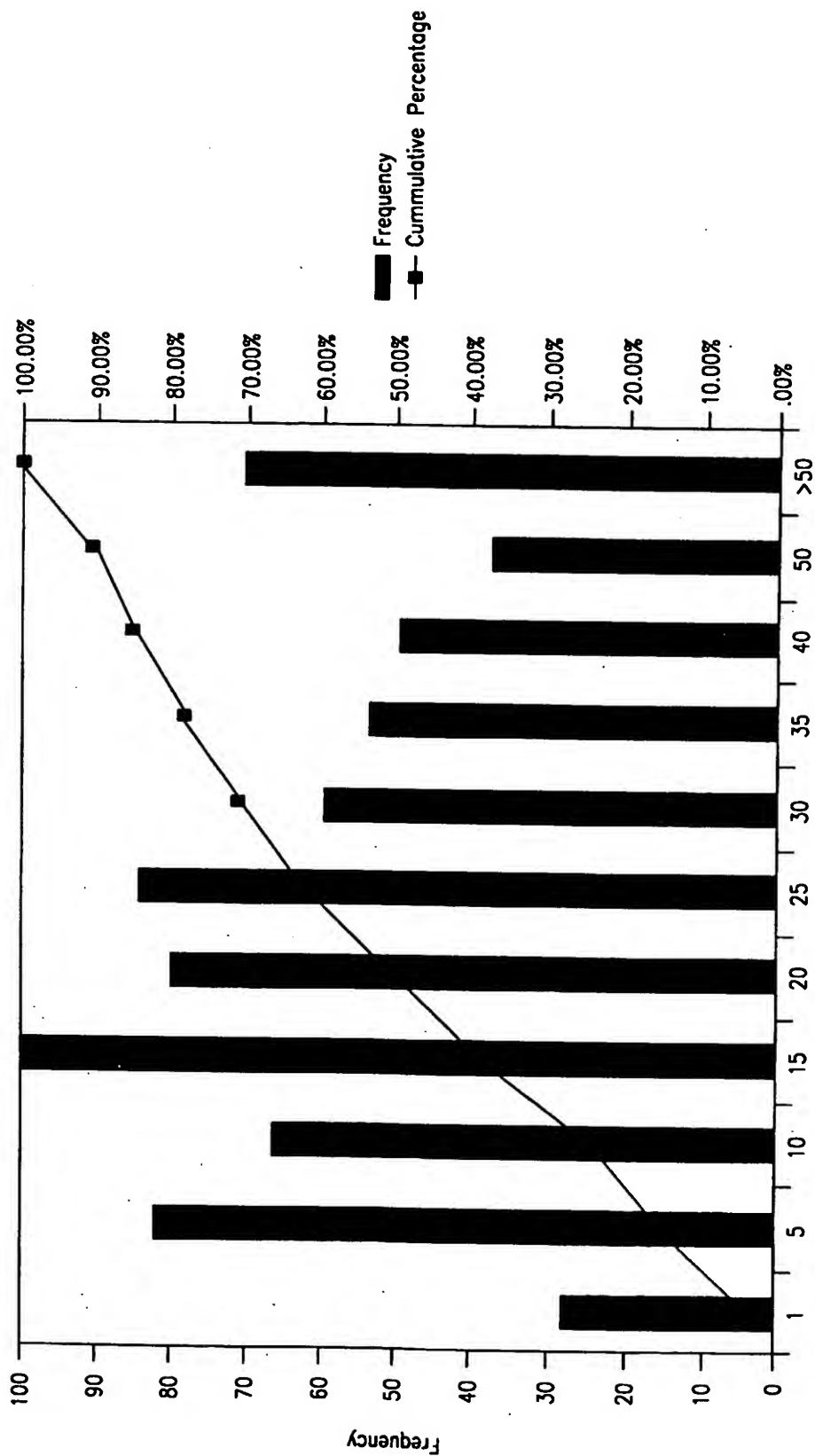


FIG. 11

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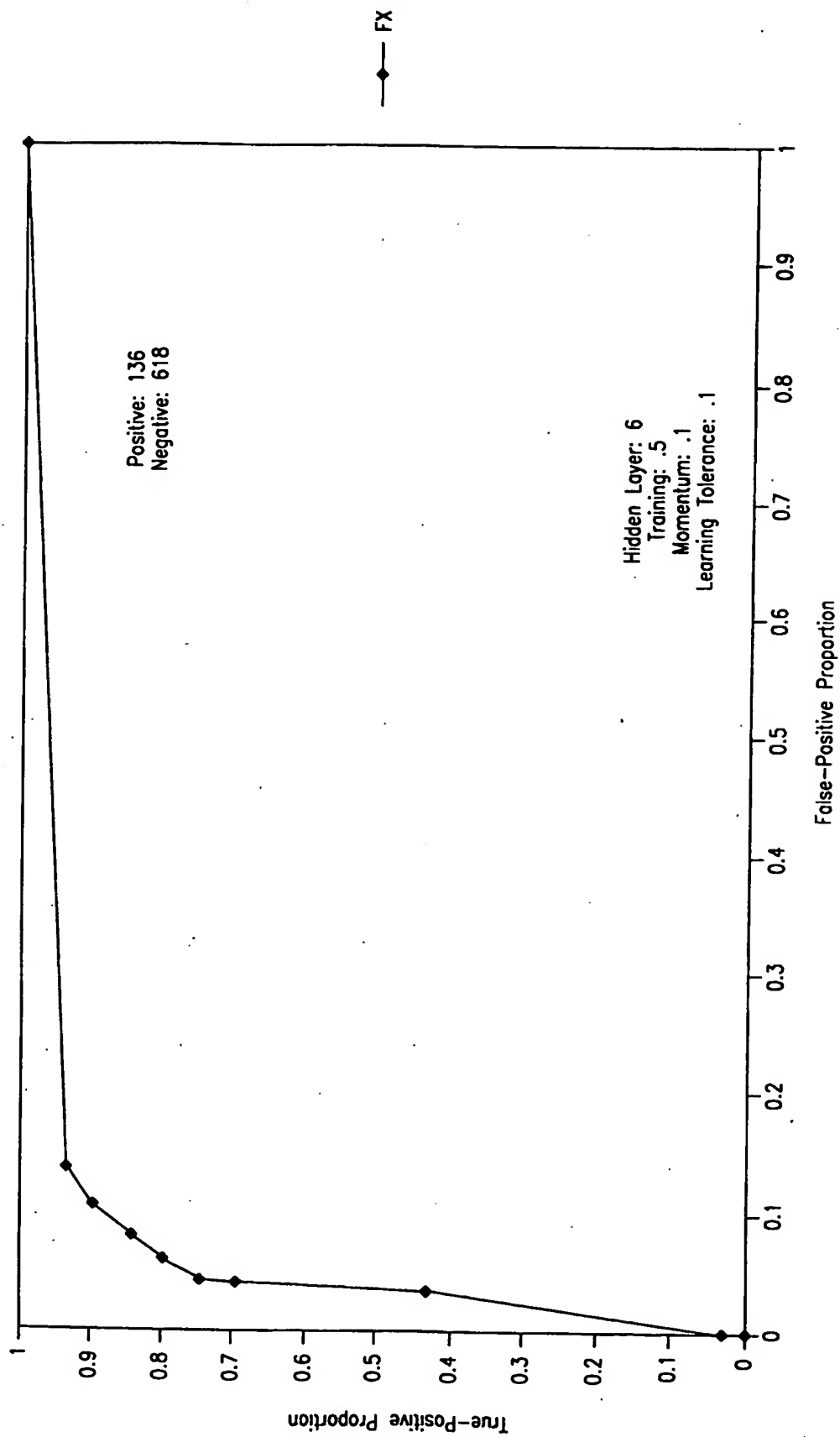


FIG. 12

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FIG. 13

Predictor Variables

Predictor Variable	Description
$p_{v,j1} = \left(\frac{dT}{dt} \right)_{\min}$	minimum of the first derivative
$p_{v,j2} = t \text{ at } \left(\frac{dT}{dt} \right)_{\min}$	time index of the minimum of the first derivative
$p_{v,j3} = \left(\frac{d^2T}{dt^2} \right)_{\min}$	minimum of the second derivative
$p_{v,j4} = t \text{ at } \left(\frac{d^2T}{dt^2} \right)_{\min}$	index of the minimum of the second derivative
$p_{v,j5} = \left(\frac{d^2T}{dt^2} \right)_{\max}$	maximum of the second derivative
$p_{v,j6} = t \text{ at } \left(\frac{d^2T}{dt^2} \right)_{\max}$	index of the maximum of the second derivative
$p_{v,j7} = T_{t0} - T_{tR}$	overall change in transmittance during the reaction

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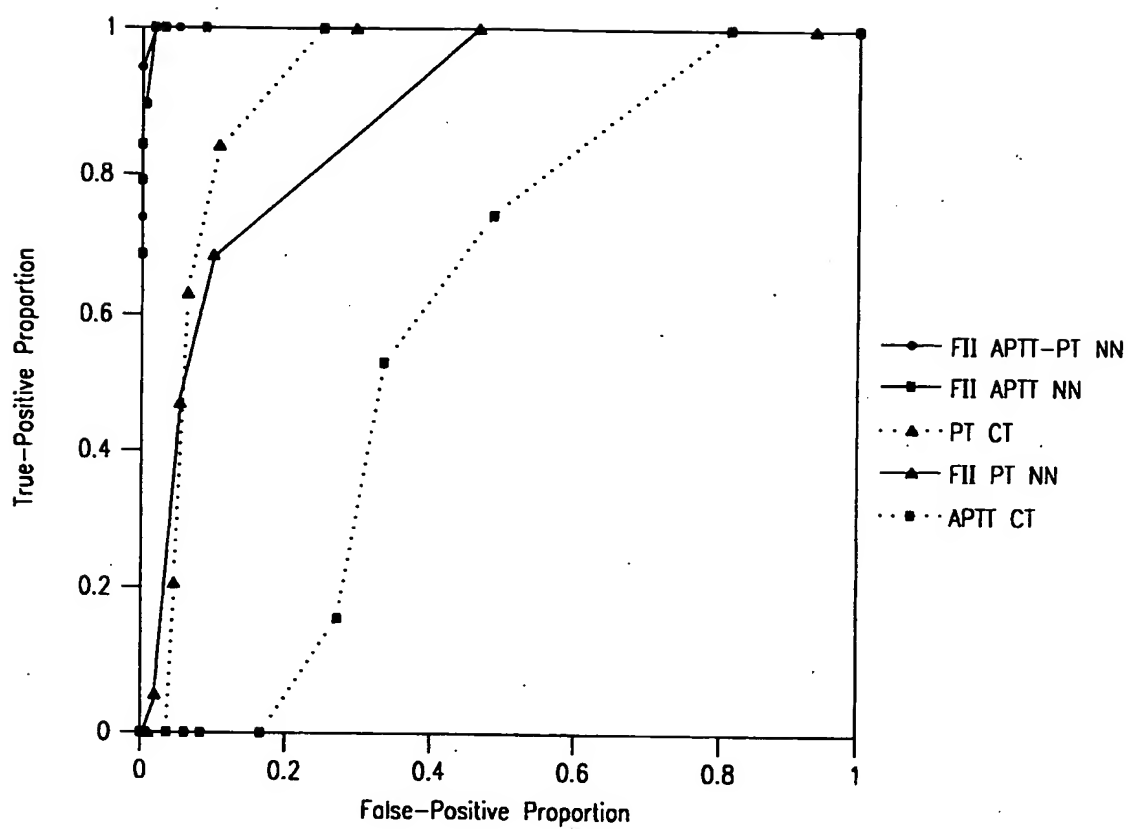


FIG. 14

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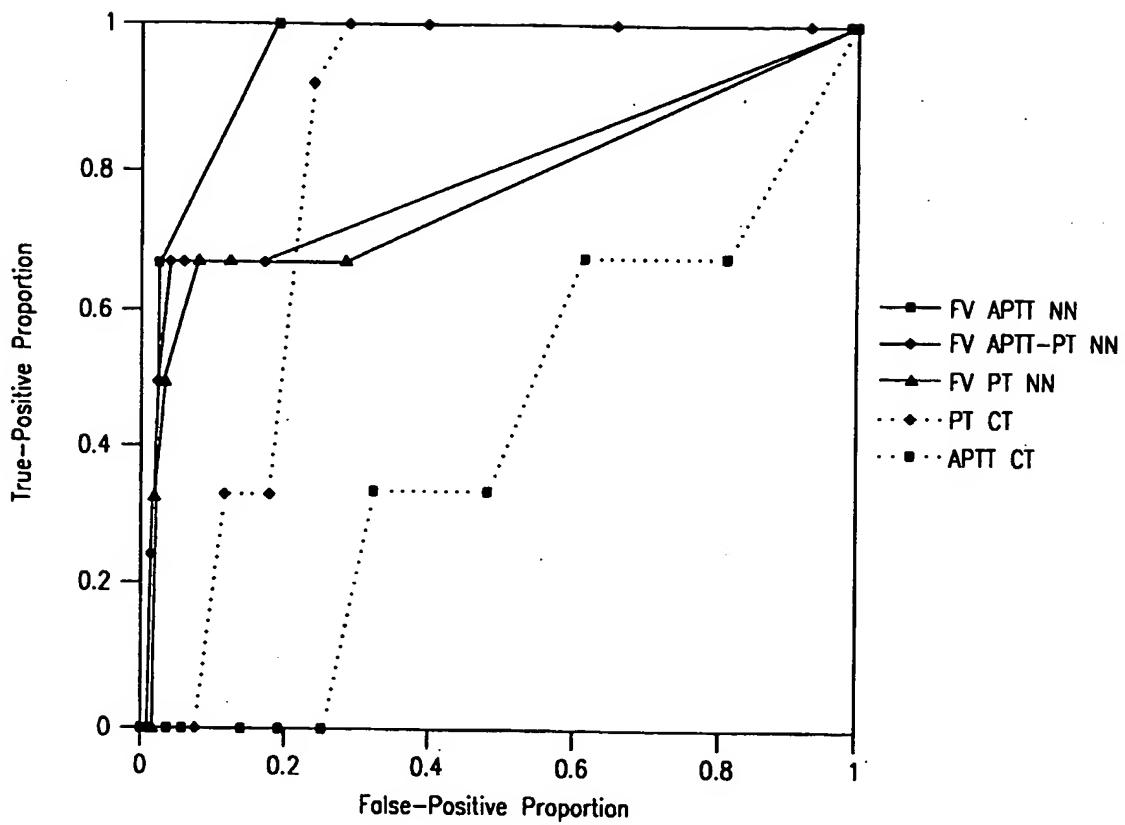


FIG. 15

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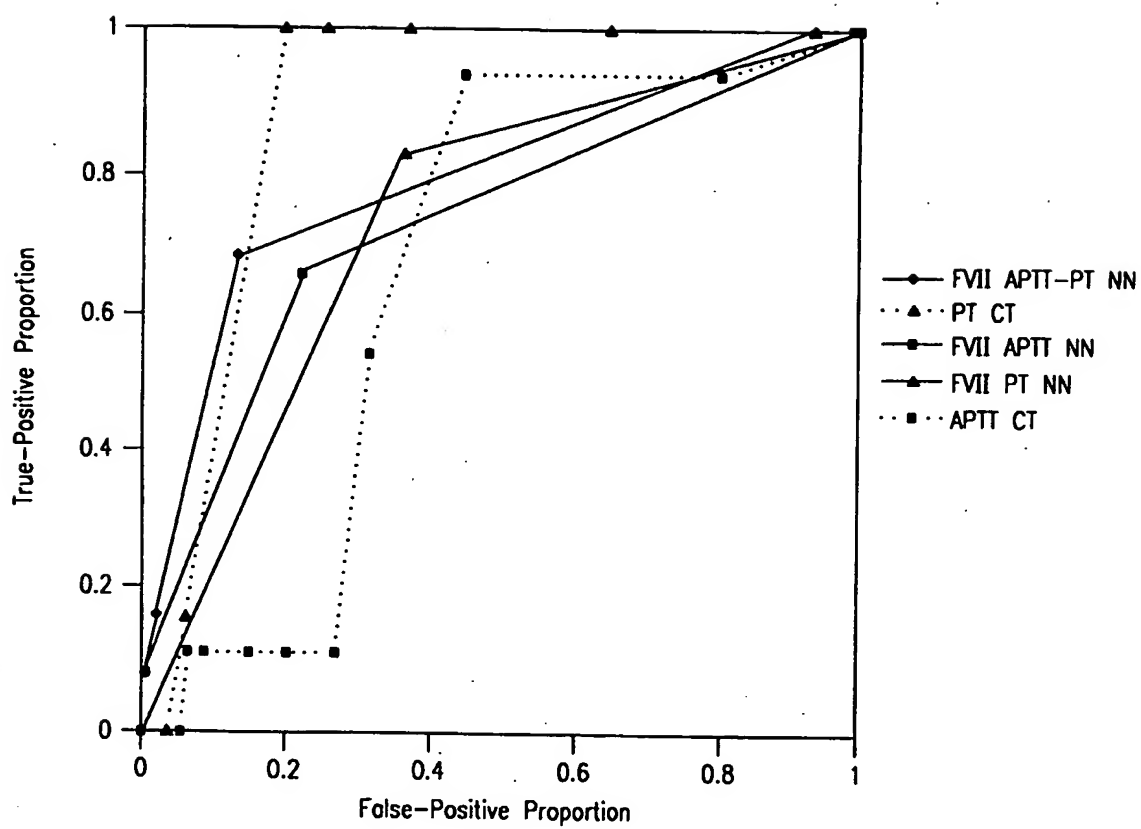


FIG. 16

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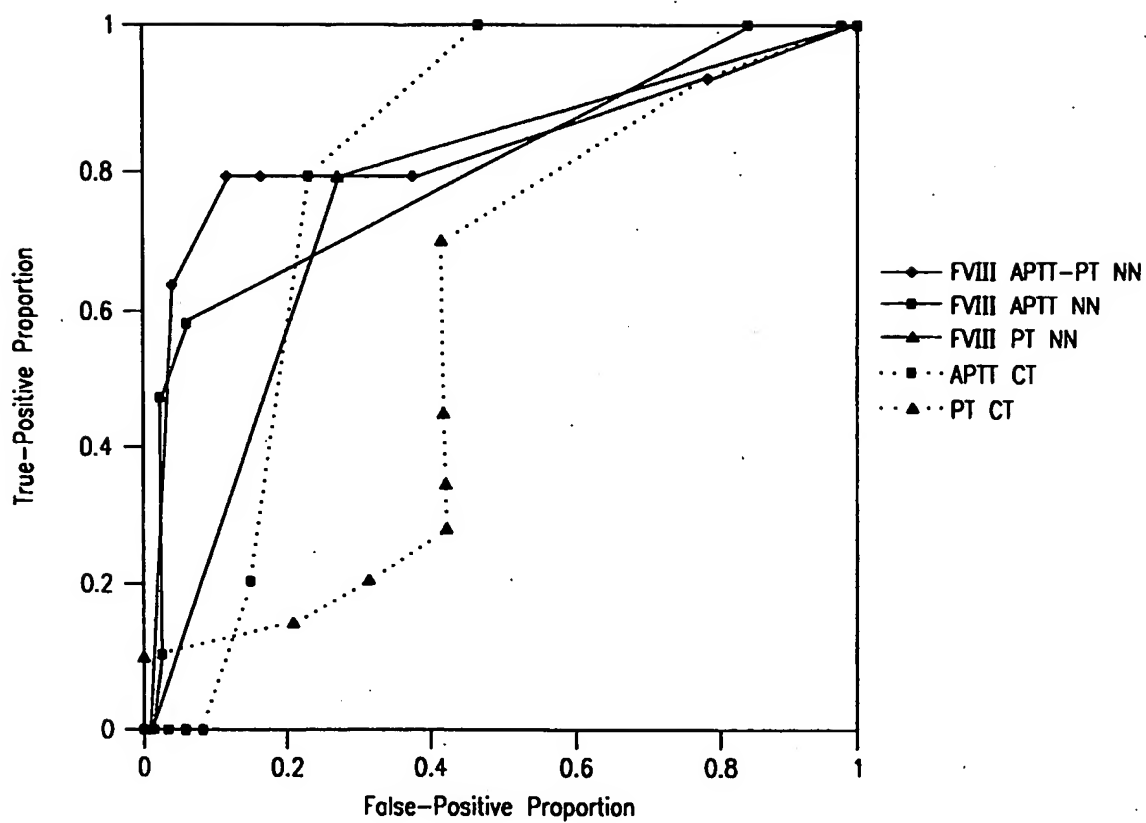


FIG. 17

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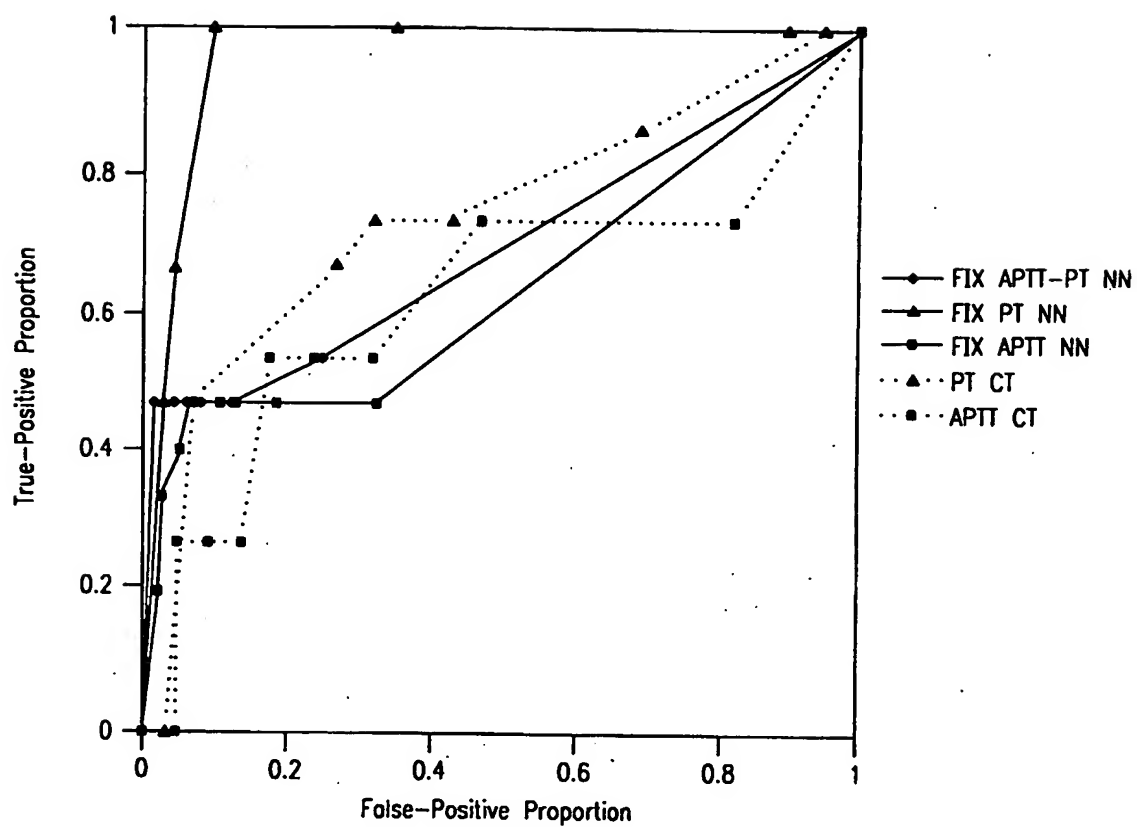


FIG. 18

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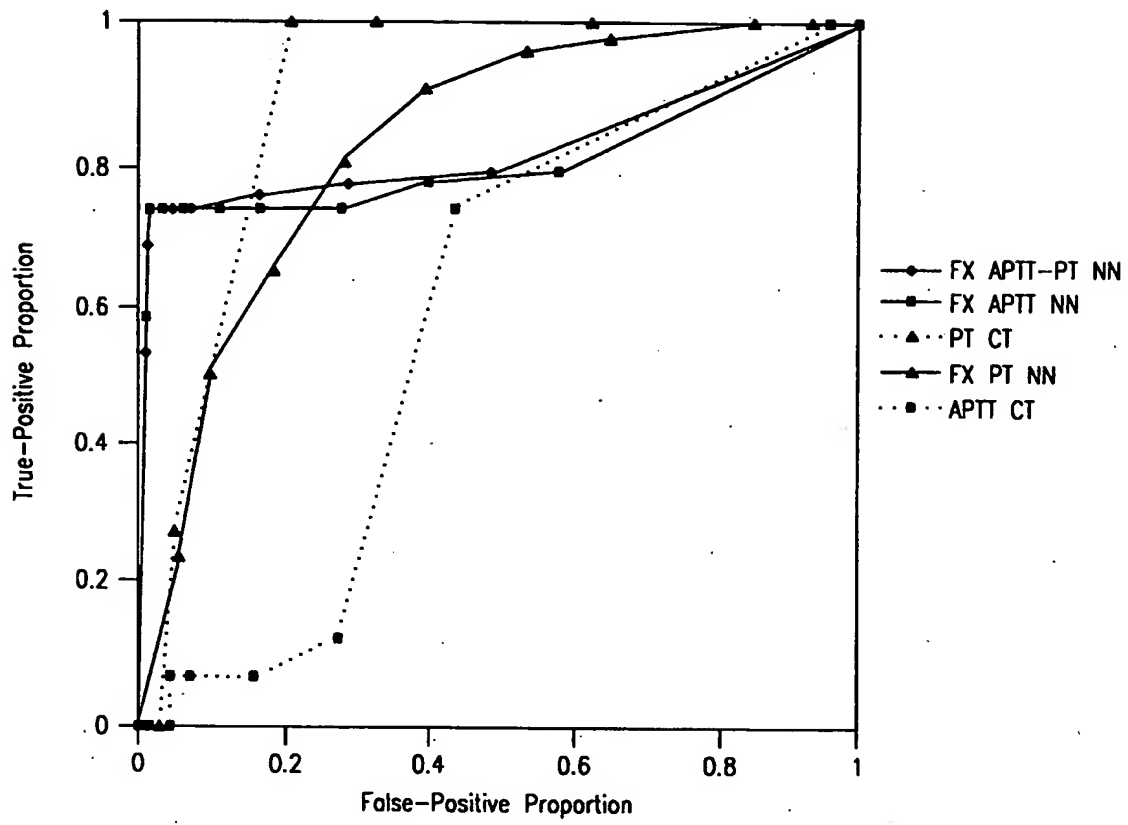


FIG. 19

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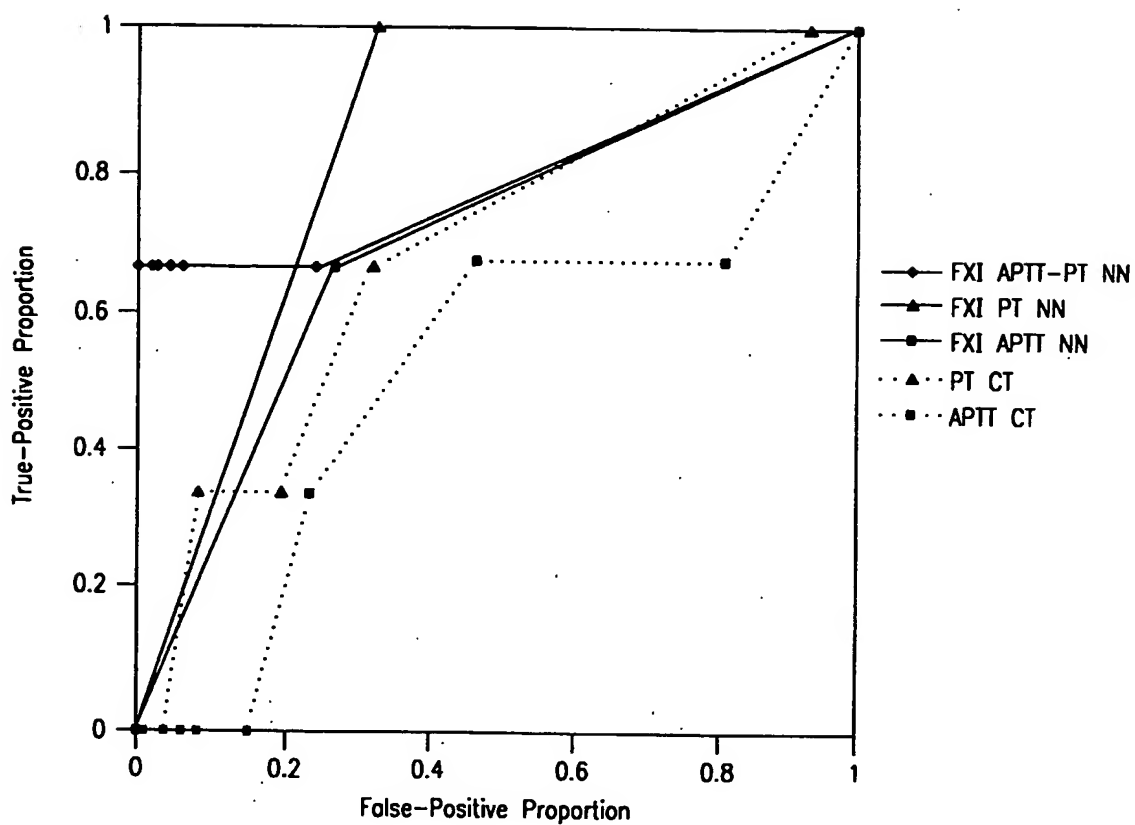


FIG. 20

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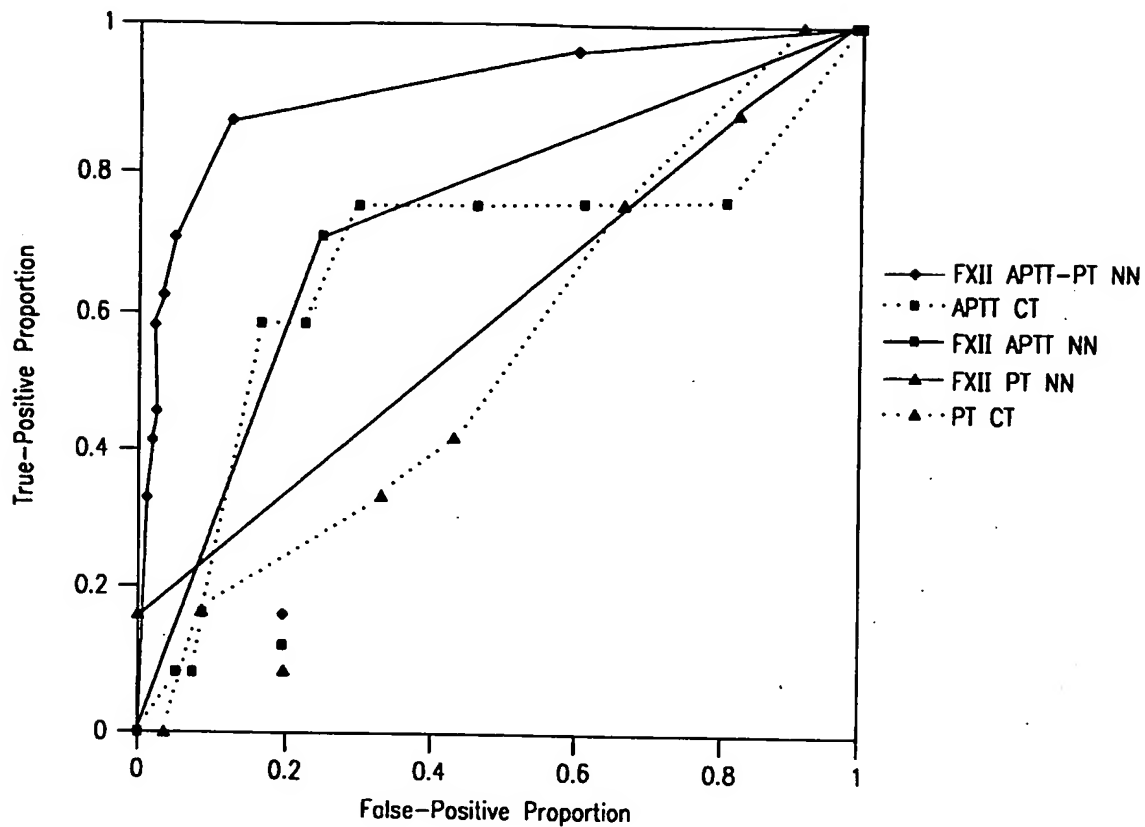


FIG. 21

Condition	Training Set		Cross-Validation Set	
	Negative	Positive	Negative	Positive
FII < 30%	346	32	362	19
FV < 30%	362	12	366	12
FVII < 30%	354	32	343	35
FVIII < 30%	342	32	367	19
FIX < 30%	344	26	360	15
FX < 30%	294	76	324	58
FX < 10%	338	32	369	13
FX < 50%	266	104	289	93
FXI < 30%	358	12	367	12
FXII < 30%	346	32	362	24

FIG. 22

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Results of classification of coagulation factor deficiencies as determined from area under ROC curves. Results are shown for classification based on APTT and PT clot times (APTT CT and PT CT, respectively) and from neural networks using APTT optical data parameter sets (APTT NN), PT data parameters (PT NN) and combined data sets from both assays (APTT-PT NN). Results are expressed as area under ROC curves and the associated standard error (SE) calculated according to [19].

Condition	APTT-PT NN		APTT NN		PT NN		APTT CT		PT CT		Comments
	Area	SE	Area	SE	Area	SE	Area	SE	Area	SE	
Factor Cut-off											
FII 30%	0.999	0.001	0.998	0.002	0.876	0.032	0.594	0.044	0.922	0.016	Best results for APTT NN, APTT-PT NN
FV 30%	0.787	0.087	0.942	0.018	0.760	0.090	0.412	0.076	0.815	0.026	Best results for APTT NN
FVII 30%	0.791	0.045	0.724	0.049	0.728	0.041	0.661	0.036	0.882	0.017	NNs do not provide either greater area under curve or higher specificity (Fig. 5)
FVIII 30%	0.826	0.065	0.794	0.060	0.752	0.055	0.789	0.027	0.423	0.082	NNs do not give greater area under curve; do tend toward higher specificity (Fig. 6)
FIX 30%	0.691	0.087	0.634	0.090	0.961	0.011	0.622	0.090	0.738	0.073	Best results for PT NN
FX 30%	0.827	0.041	0.809	0.043	0.830	0.025	0.579	0.034	0.894	0.016	NNs do not give greater area under curve; do tend toward higher specificity (Fig. 11)
FXI 30%	0.790	0.093	0.692	0.080	0.826	0.033	0.509	0.091	0.675	0.077	Best results for APTT-PT NN if greater specificity is desired (Fig. 8)
FXII 30%	0.902	0.039	0.710	0.055	0.586	0.067	0.659	0.070	0.530	0.058	Best results for APTT-PT NN

FIG. 23

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Areas under ROC curves for three networks trained to classify factor deficiencies based on three different diagnostics cutoffs (10%, 30%, and 50%). The area under the ROC curve for PT clot time is also included. ROC curves for APTT clot time are not shown due to the generally accepted insensitivity of APTT clot time to FX (as exhibited in Table II). SE is the standard error associated with the area.

Condition		APTT-PT NN		PT CT	
Factor	Cut-off	Area	SE	Area	SE
FX < 10%		0.994	0.004	0.951	0.016
FX < 30%		0.827	0.041	0.894	0.016
FX < 50%		0.748	0.035	0.900	0.016

FIG. 24

Results from linear regressions comparing factor concentrations estimated using neural networks with measured factor concentrations, including the slope, intercept, and the Pearson product moment correlation coefficient (r). Pearson correlation coefficients are also included for linear regressions comparing APTT and PT clot times with measured factor concentrations.

Factor	APTT-PT NN			APTT Clot Time	PT Clot Time
	Slope	Intercept	r	r	r
FII	0.53	46.7	0.62	0.05	0.05
FV	0.31	64.2	0.45	0.07	0.01
FVII	0.18	8.5	0.32	0.17	0.08
FVIII	-0.14	140.5	0.02	0.15	0.13
FIX	0.38	60.7	0.54	0.26	0.15
FX	0.50	53.2	0.60	0.11	0.13
FXI	0.20	75.4	0.37	0.27	0.08
FXII	0.35	54.8	0.51	0.10	0.08
Fibrinogen	0.89	61.9	0.97	0.07	0.07

FIG. 25

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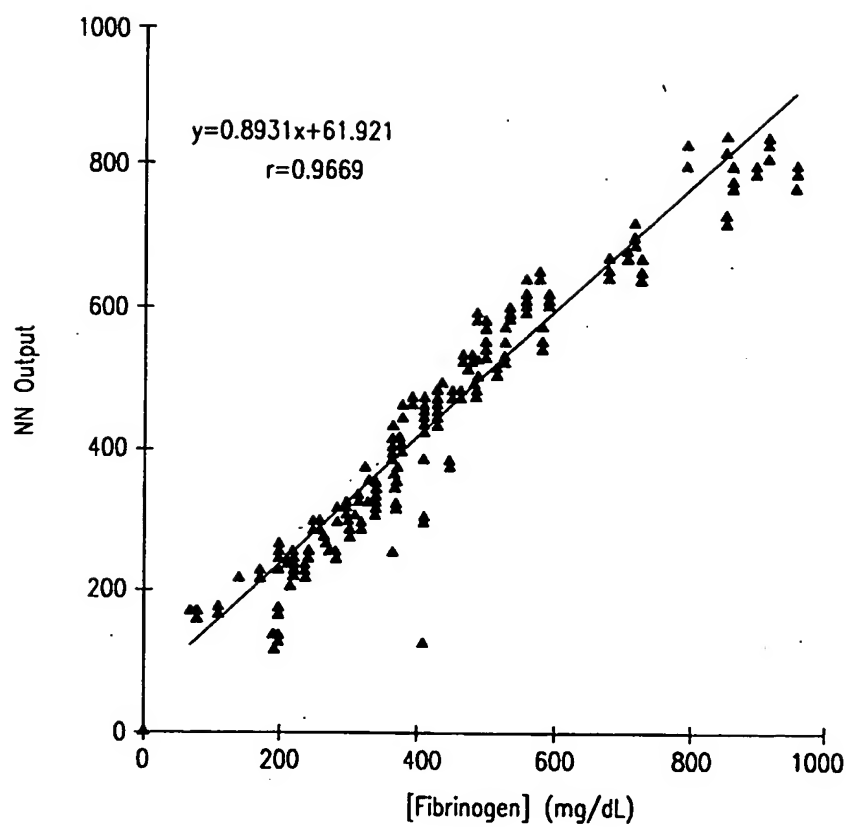


FIG. 26

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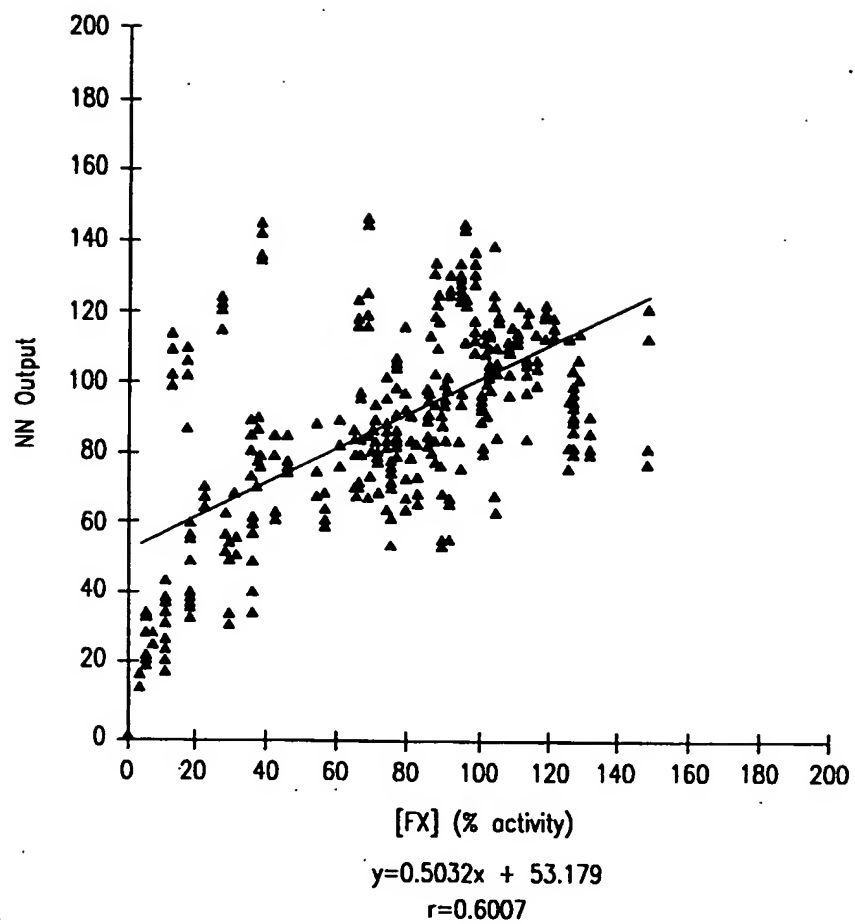


FIG. 27

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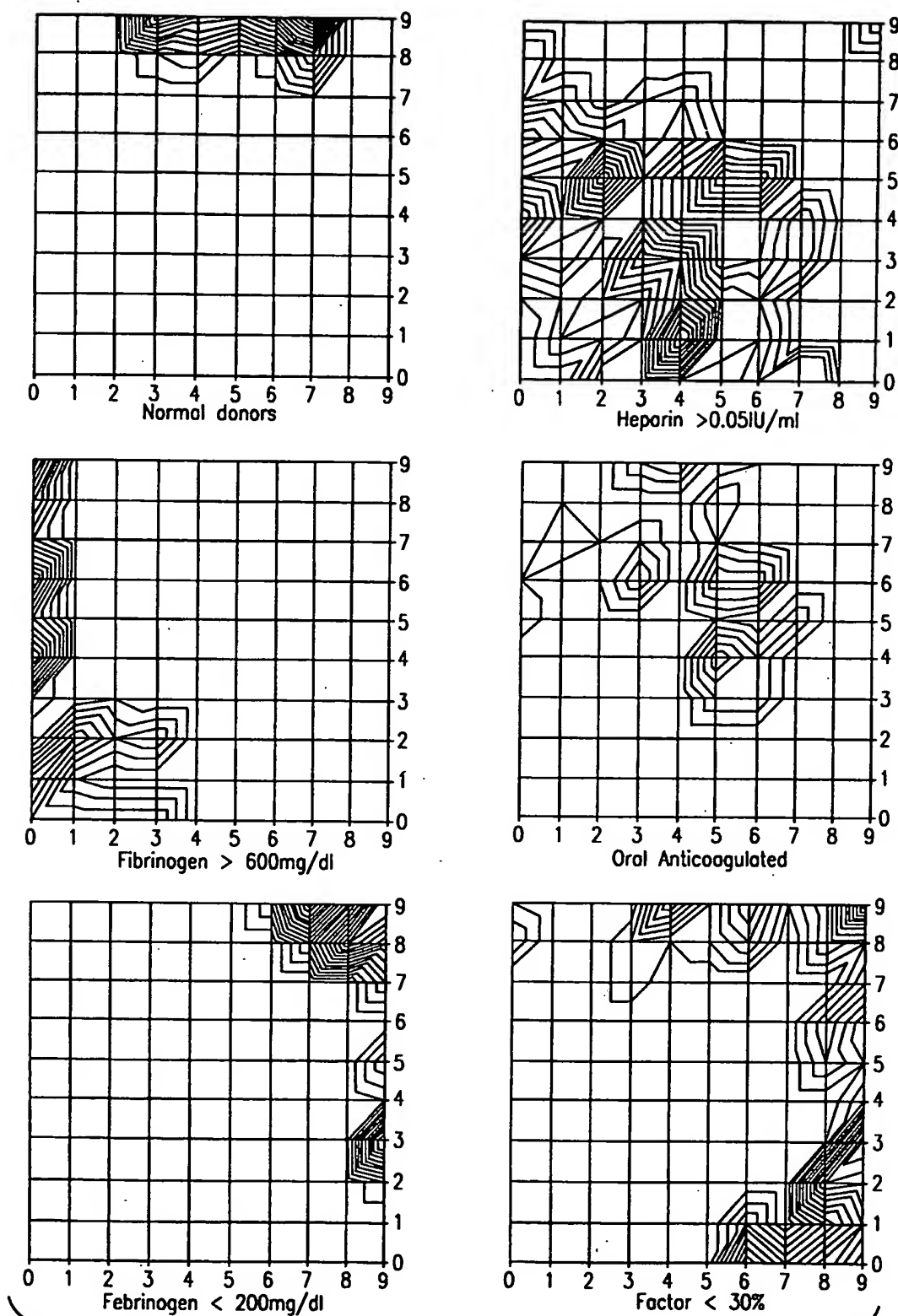


FIG. 28

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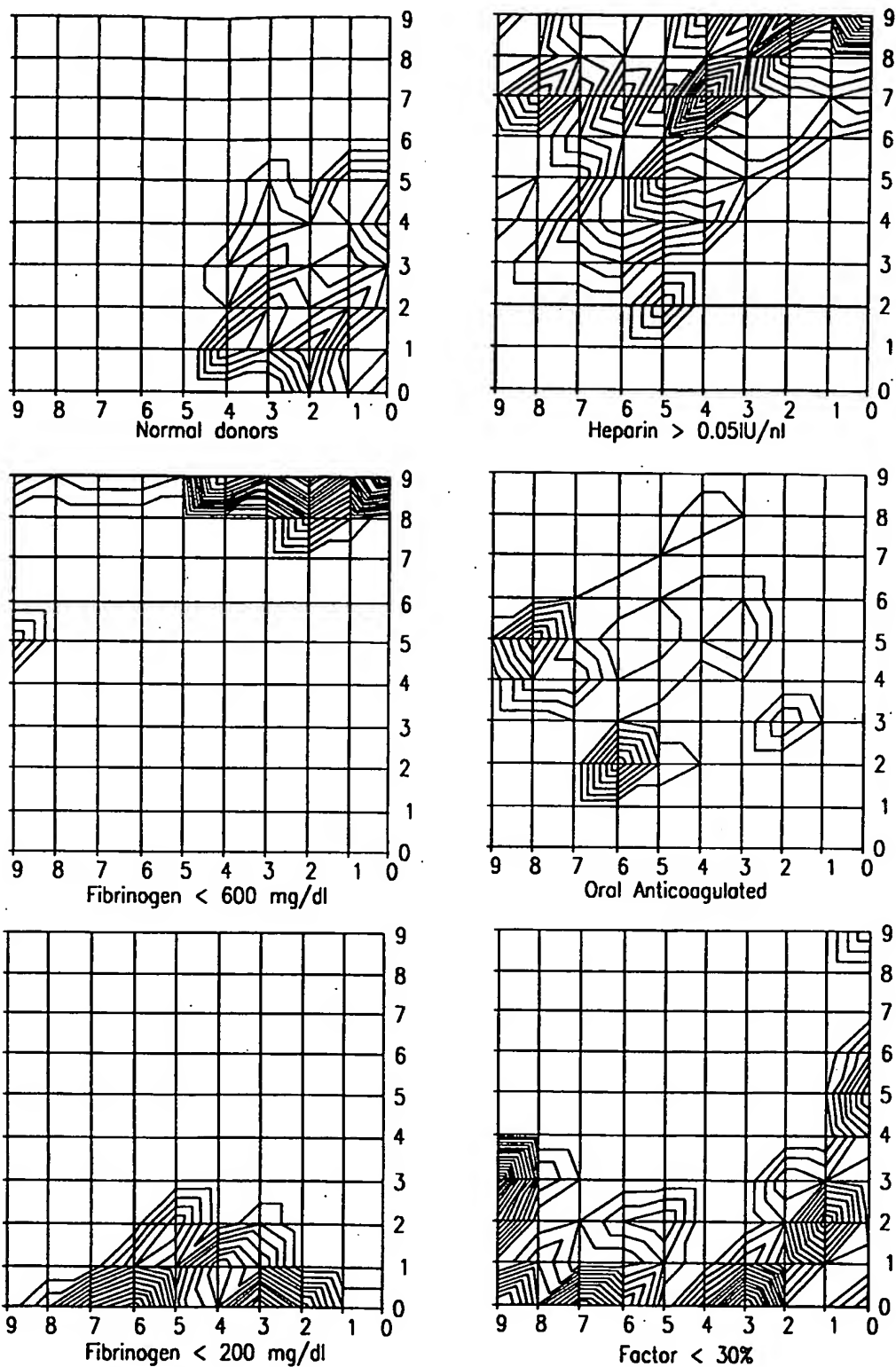


FIG. 29

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Sensitivity, specificity, efficiency, predictive value of positive test (PPV), and predictive power of negative test (NPV) for self-organizing feature maps trained using learning vector quantization to predict factor-deficiencies or heparin therapy based on either APTT or PT parameters.

Deficiency or Condition	APTT					PT				
	Sensitivity	Specificity	PPV	NPV	Efficiency	Sensitivity	Specificity	PPV	NPV	Efficiency
FII < 30%	0.84	0.93	0.39	0.99	0.93	0.79	0.96	0.51	0.99	0.95
FV < 30%	0.00	0.98	0.00	0.97	0.95	0.00	0.99	0.00	0.97	0.96
FVII < 30%	0.22	0.97	0.42	0.92	0.90	0.03	0.97	0.09	0.91	0.88
FVIII < 30%	0.33	0.96	0.21	0.98	0.94	0.00	0.96	0.00	0.97	0.93
FIX < 30%	0.47	0.91	0.18	0.98	0.89	0.00	0.96	0.00	0.96	0.92
FX < 30%	0.62	0.85	0.43	0.93	0.82	0.66	0.86	0.46	0.93	0.83
FXI < 30%	0.67	0.96	0.35	0.99	0.95	1.00	0.96	0.45	1.00	0.96
FXII < 30%	0.79	0.90	0.34	0.98	0.89	0.50	0.92	0.29	0.97	0.89
Heparin < 0.051 U/ml	0.76	0.86	0.72	0.88	0.83	0.77	0.74	0.59	0.87	0.75

FIG. 30

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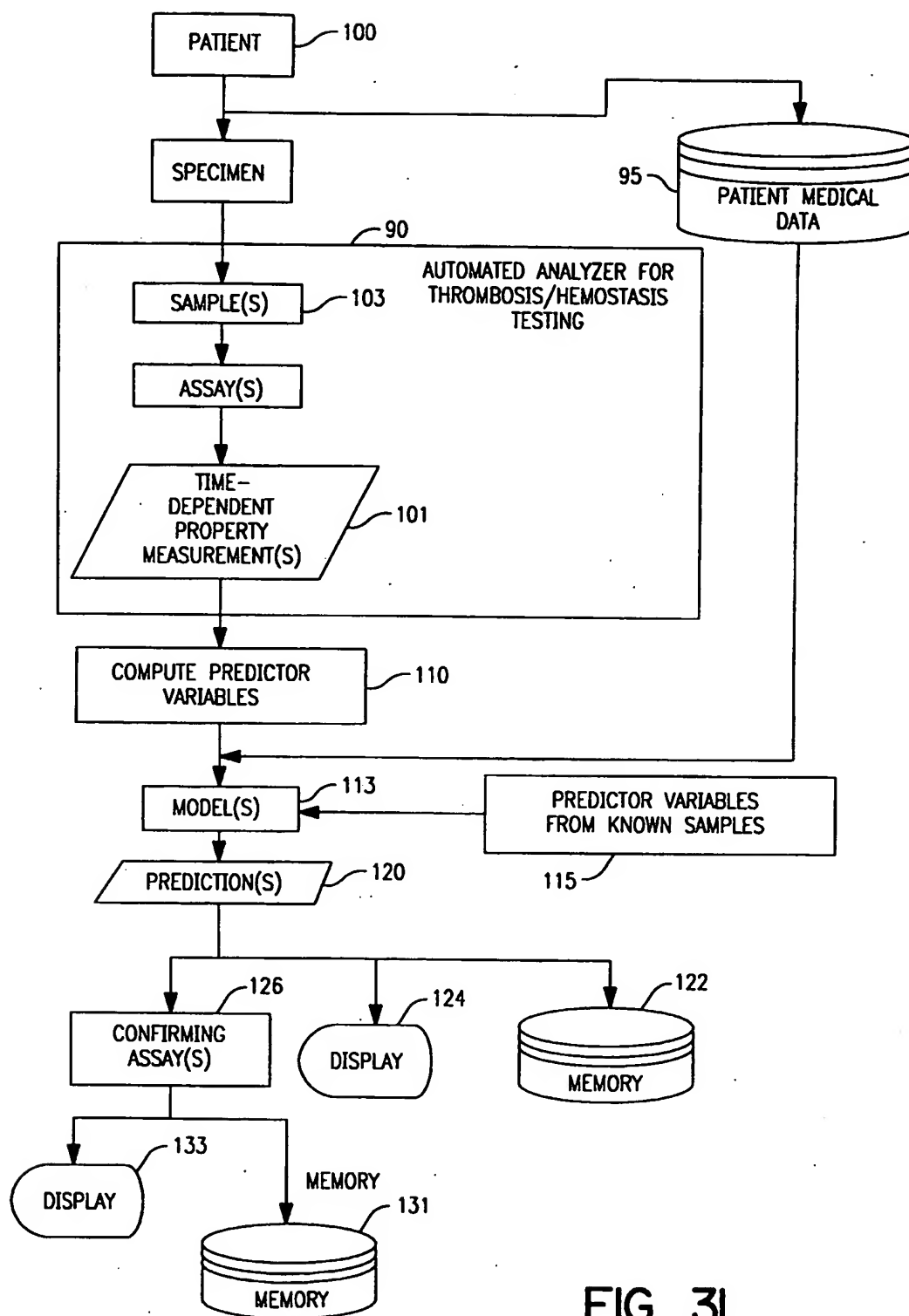


FIG. 31

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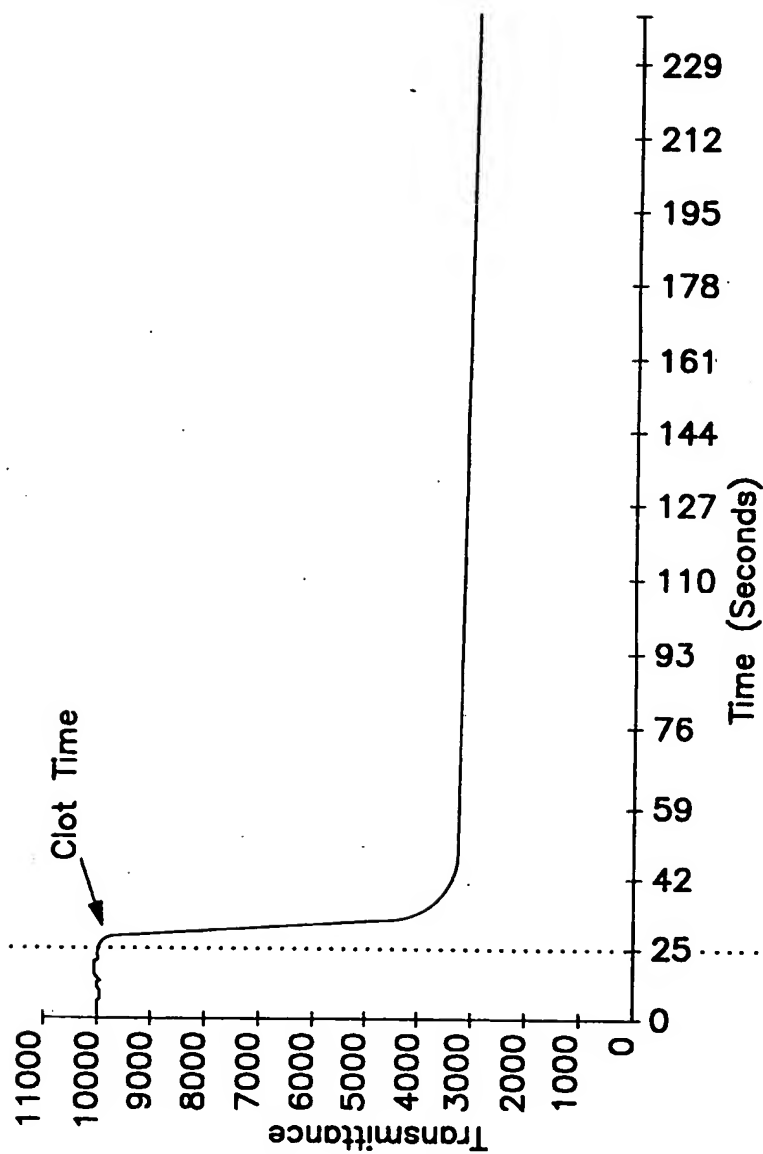


FIG. 32A

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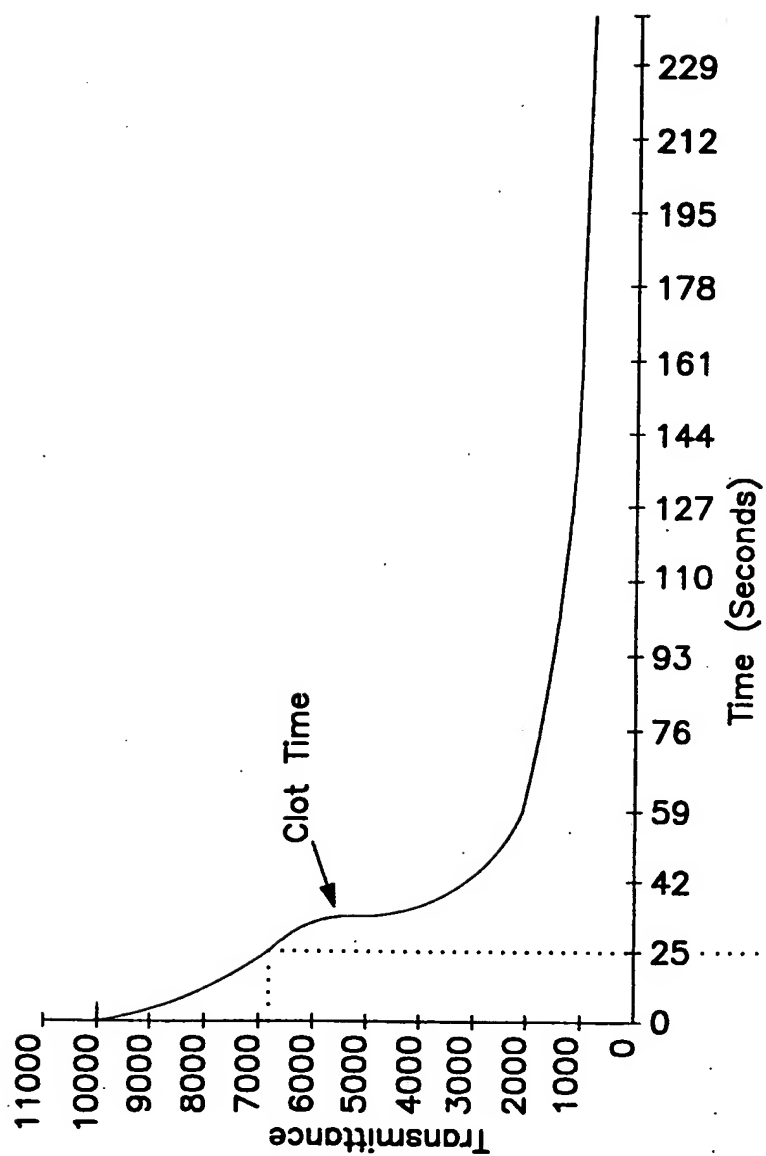


FIG. 32B

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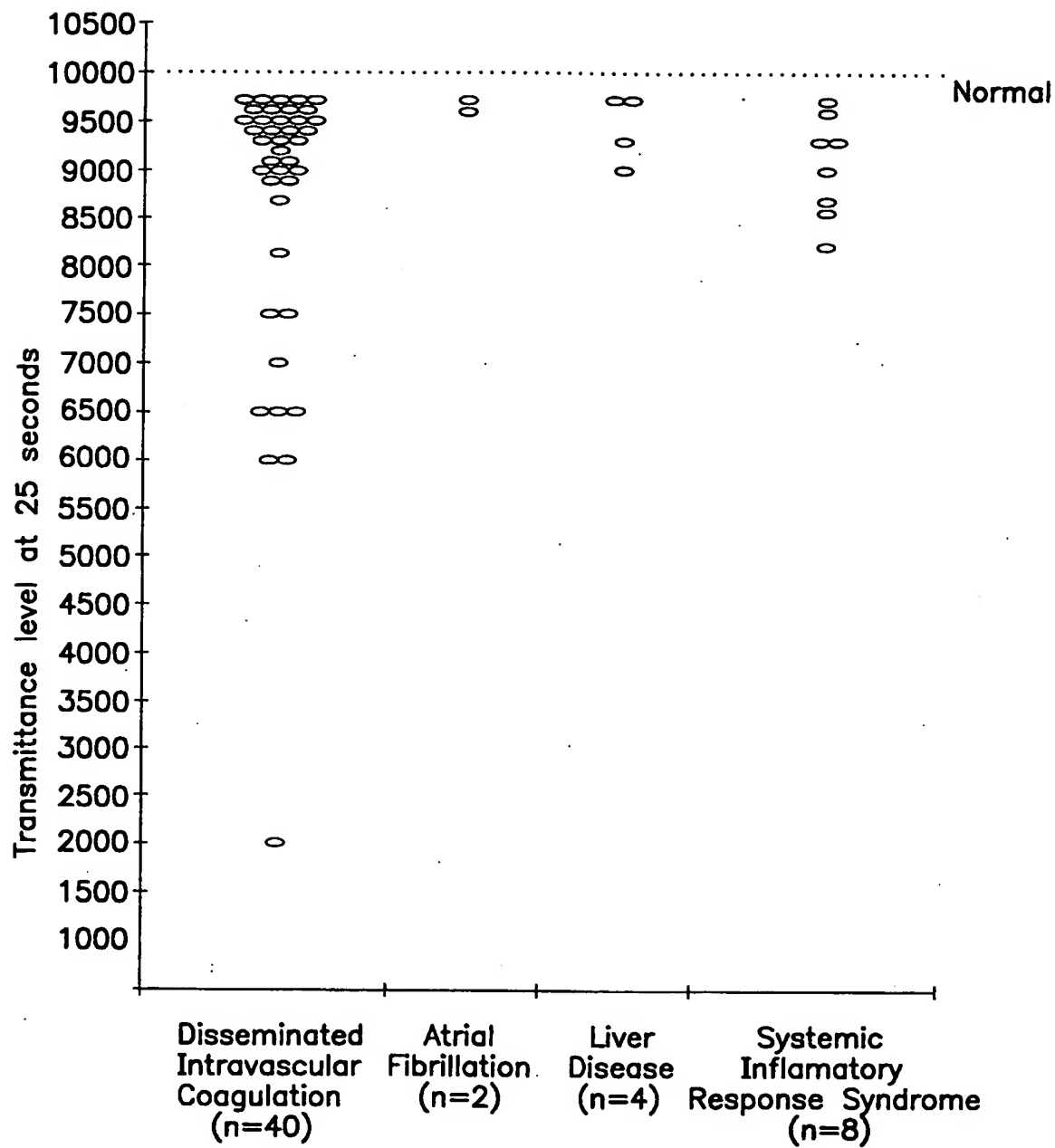


FIG. 33

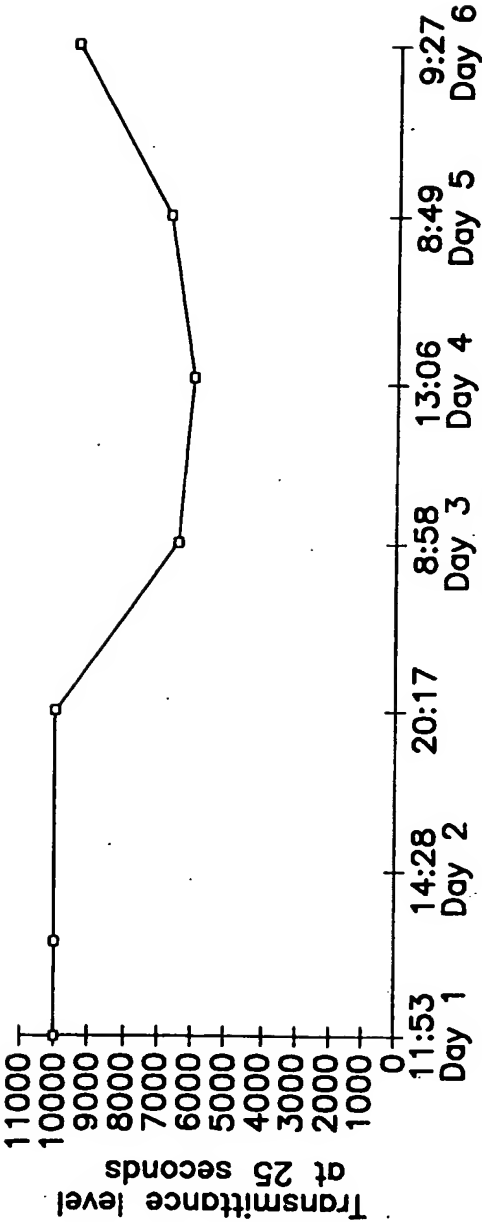


FIG. 34A

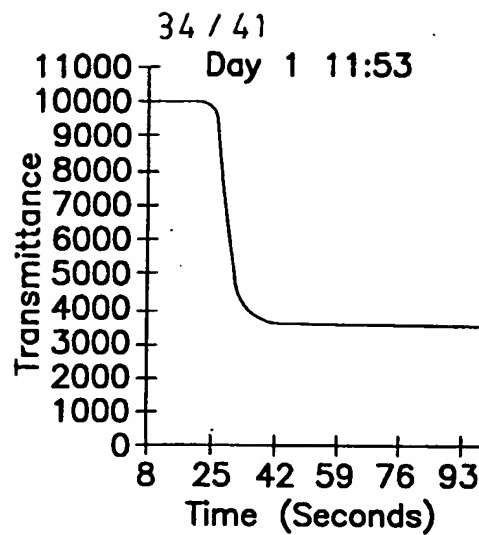


FIG. 34B

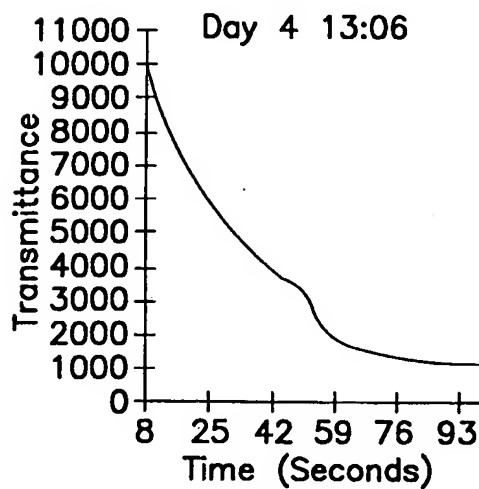


FIG. 34C

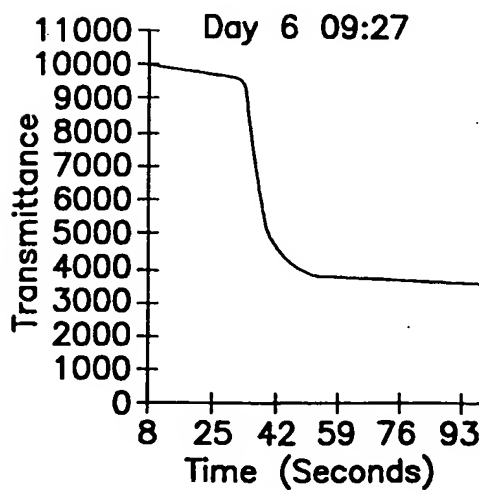


FIG. 34D

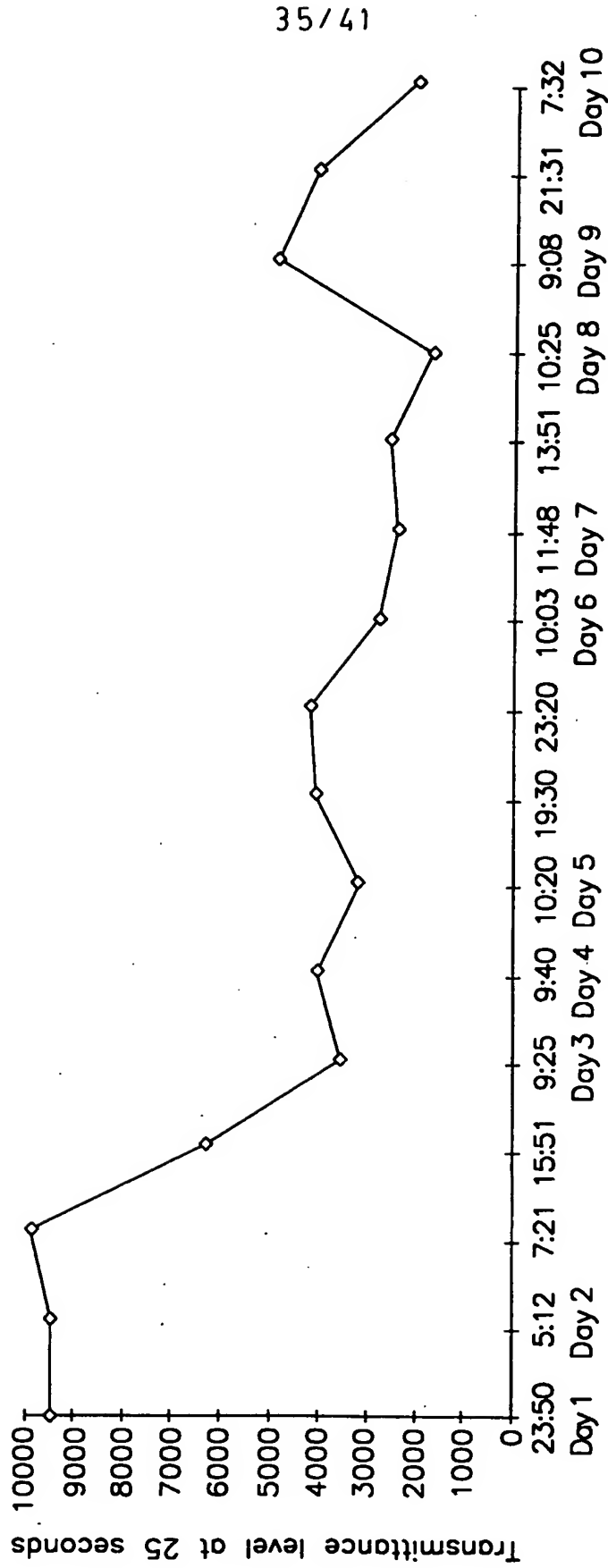


FIG. 35A

FIG. 35B

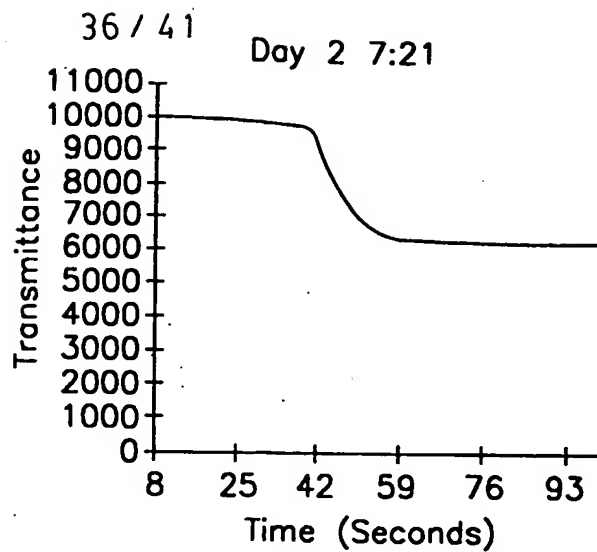


FIG. 35C

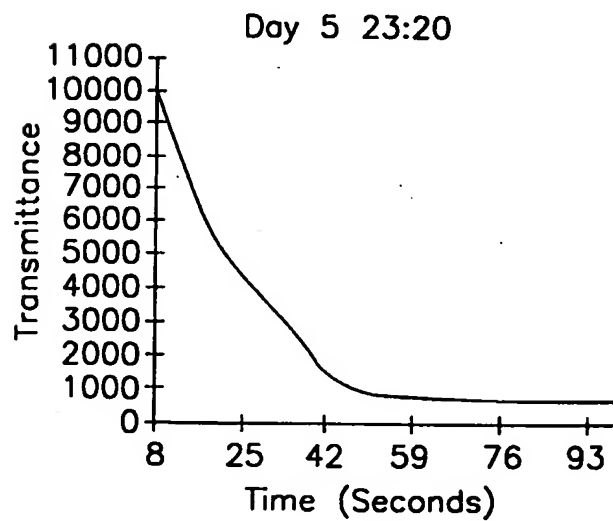
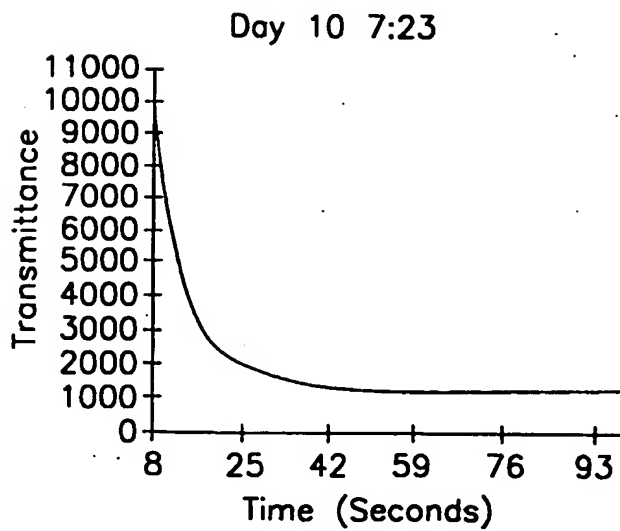


FIG. 35D



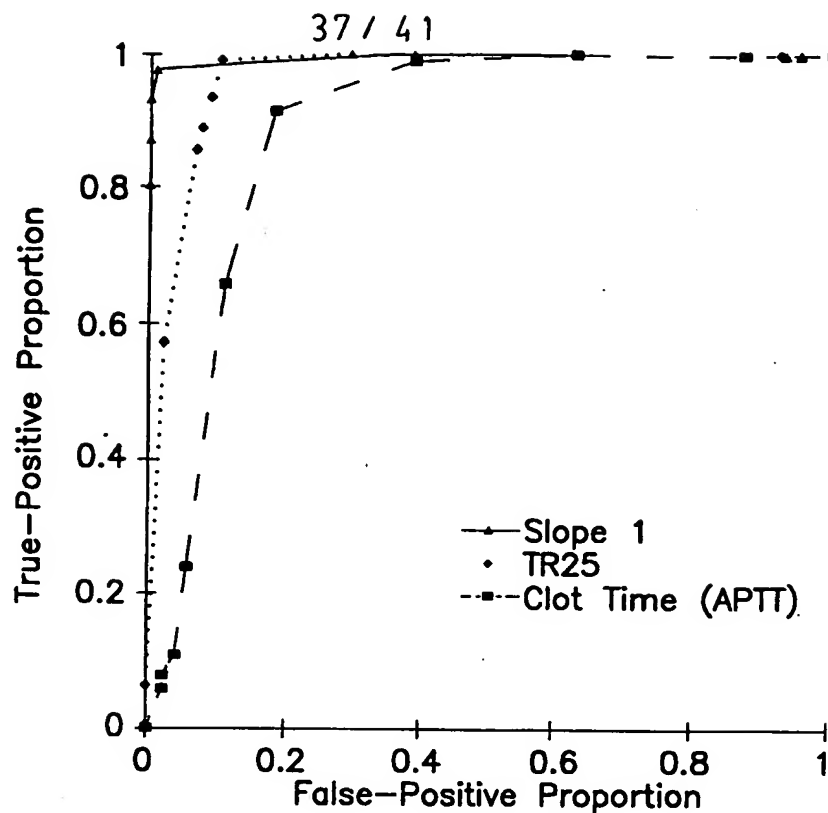


FIG. 36

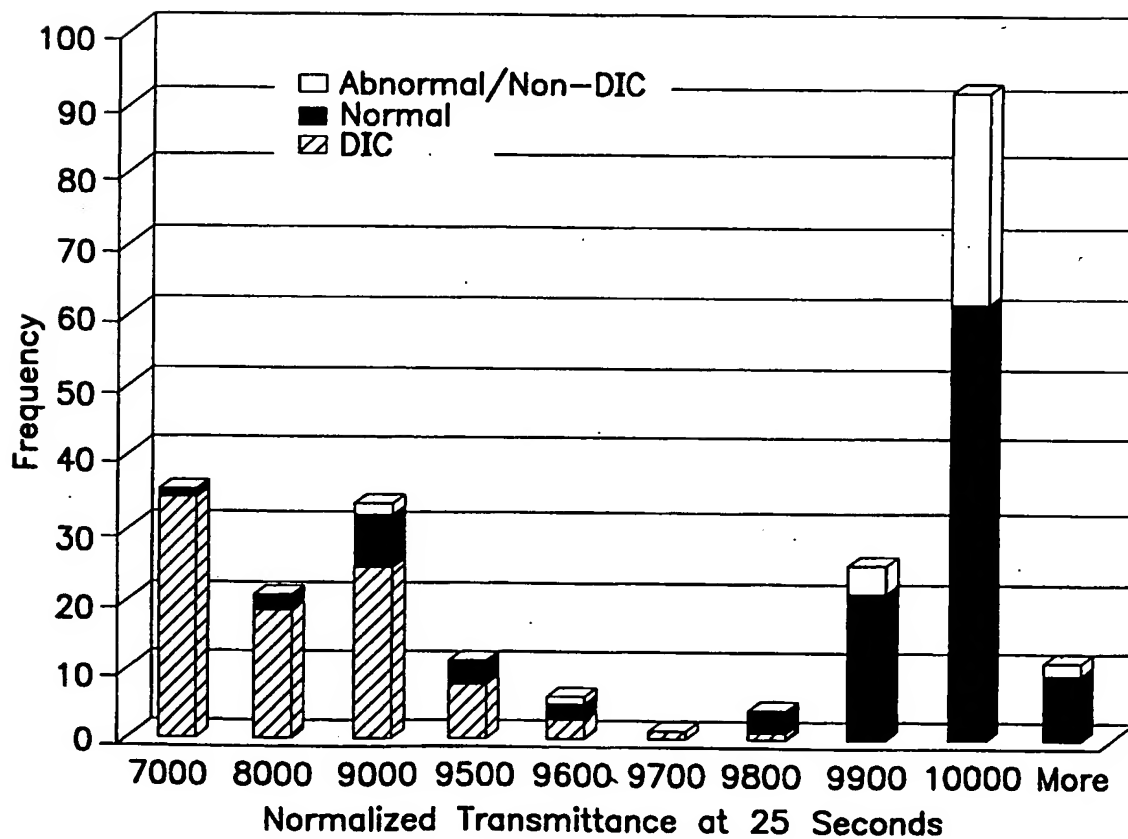


FIG. 37

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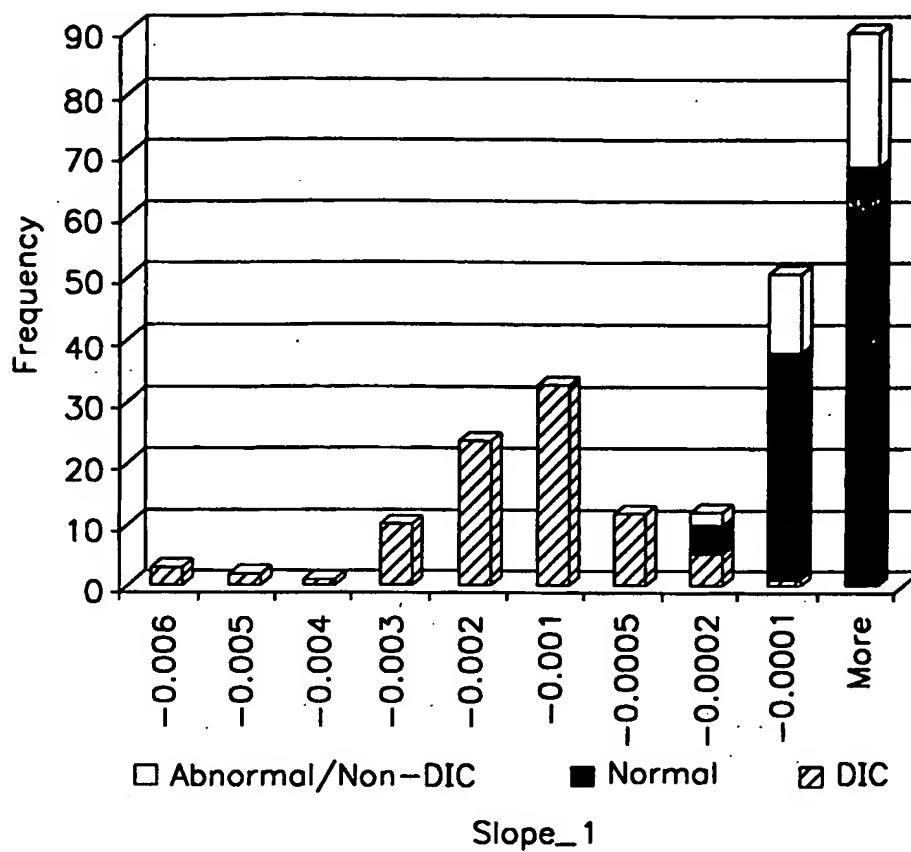


FIG. 38

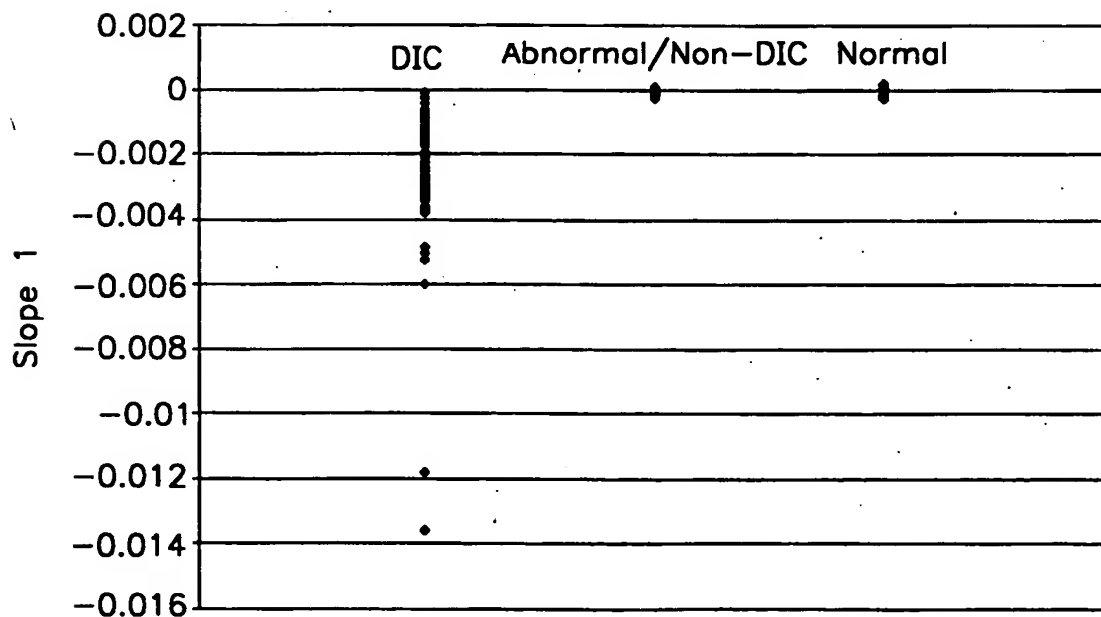


FIG. 39

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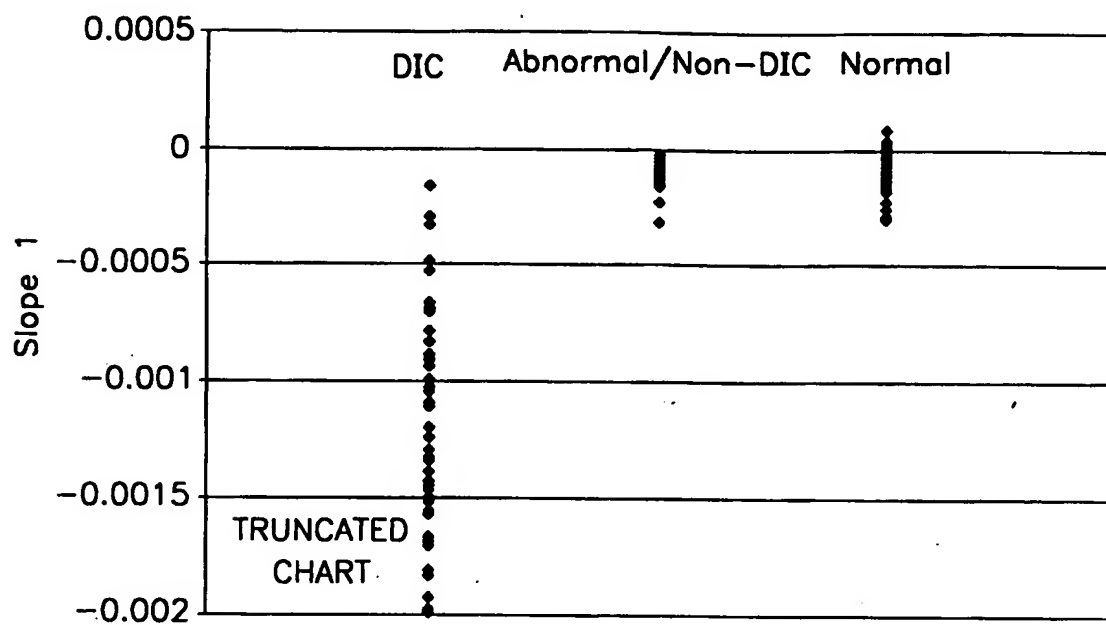


FIG. 40

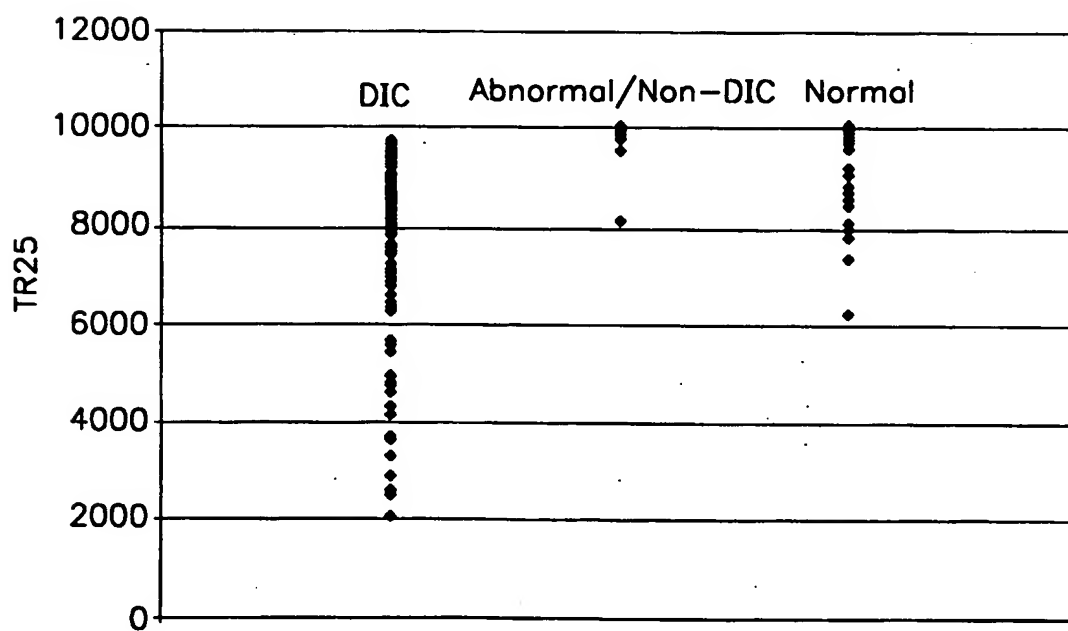


FIG. 41

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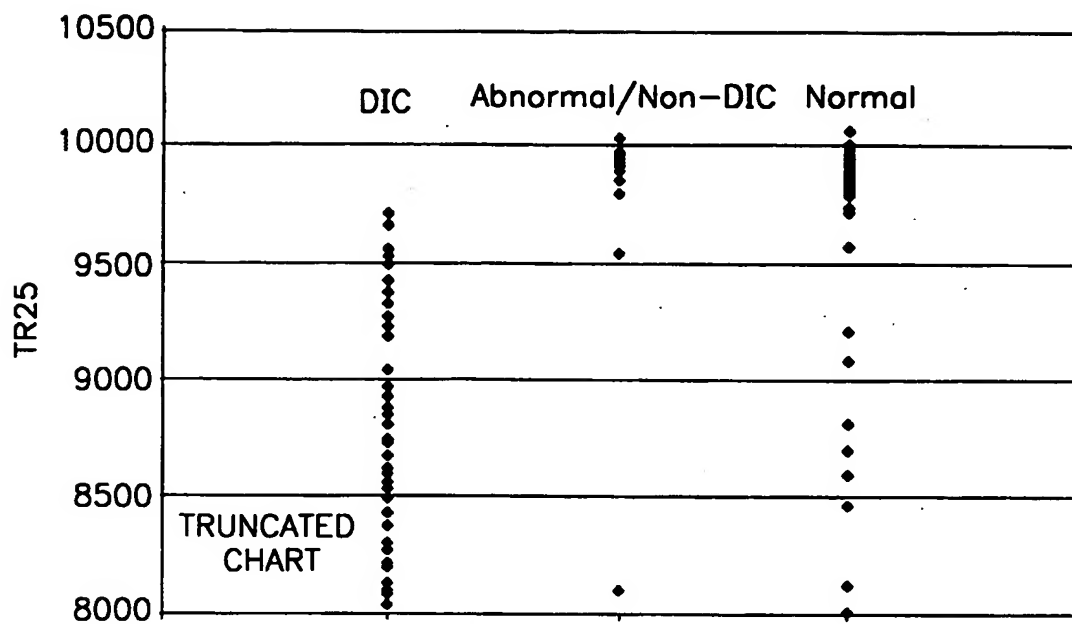


FIG. 42

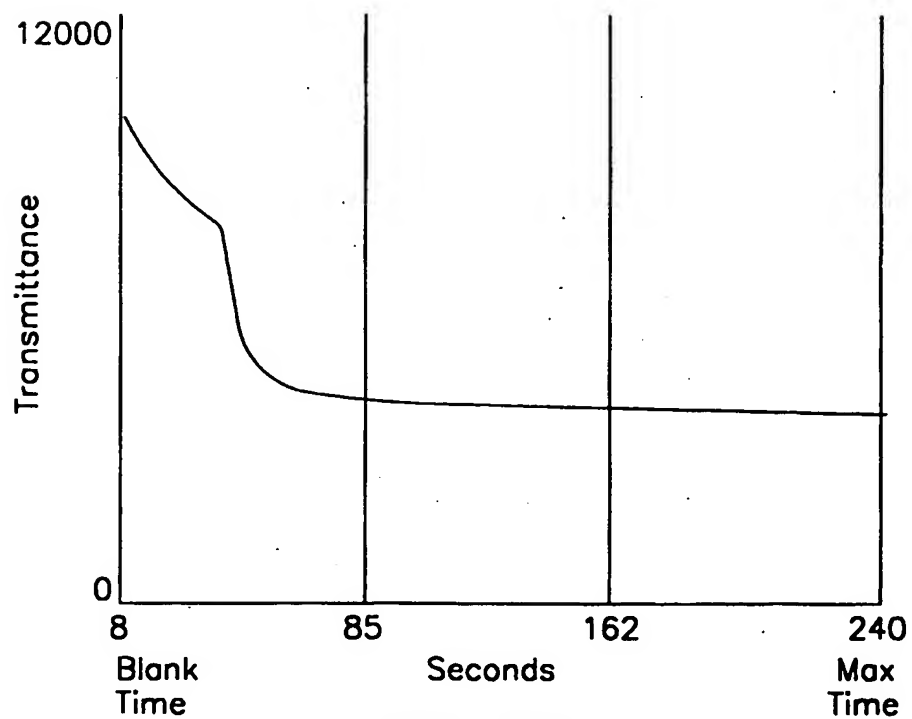


FIG. 43

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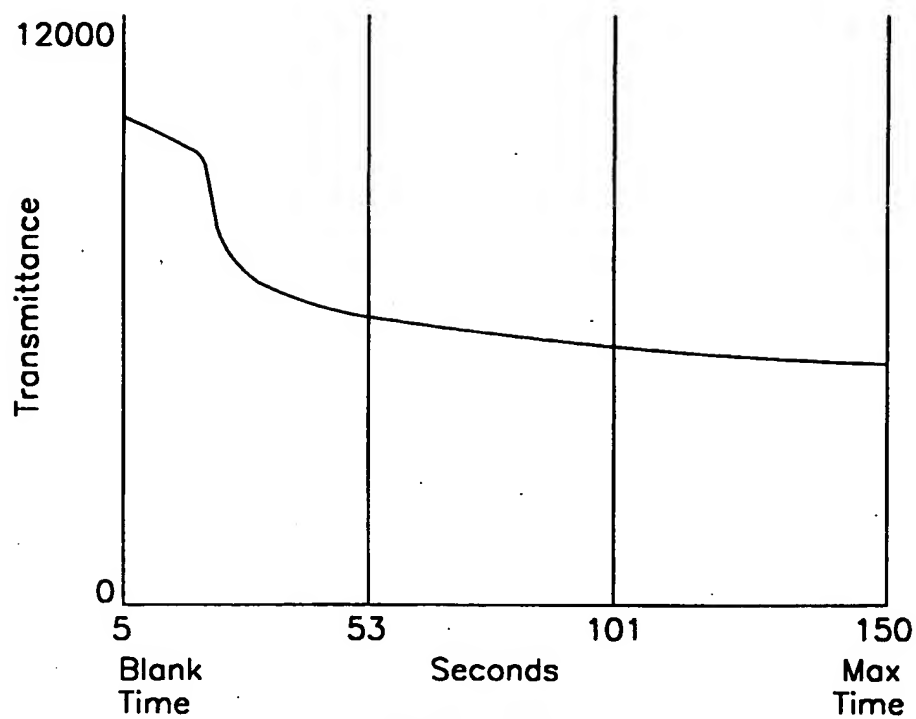


FIG. 44

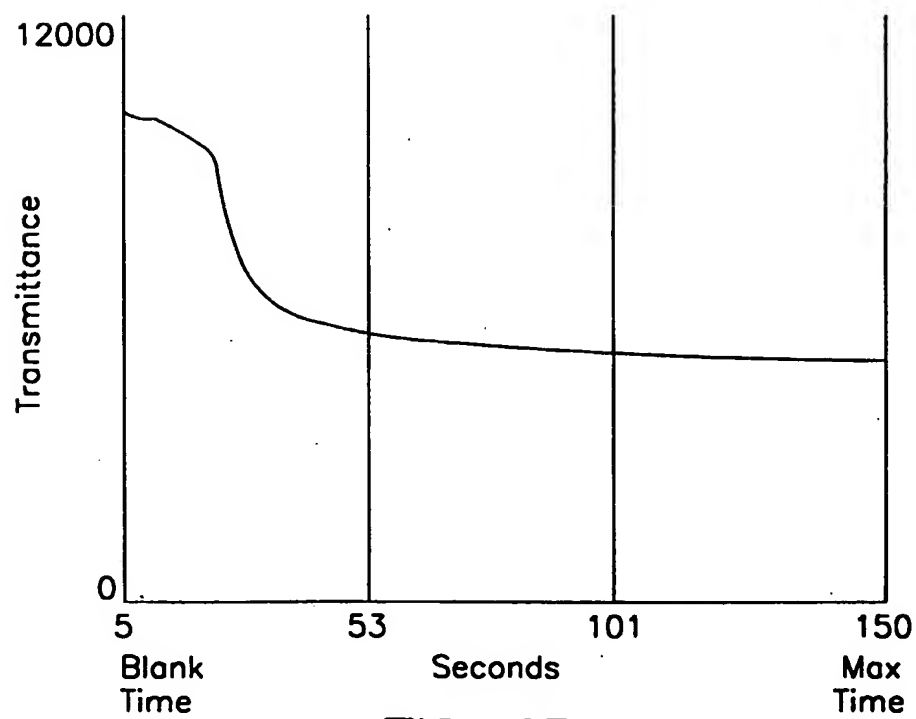


FIG. 45

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/02987**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(7) :G01N 33/86

US CL :702/22, 28, 30, 32; 703/11; 706/21

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : Please See Extra Sheet.

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
NONE

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

USPTO APS EAST

search terms: predict, haemostatic, dysfunction, profiles, model

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X — Y — A	US 5,708,591 A (GIVENS et al) 13 January 1998 (13-01-1998), abstract, figures 2, 3, 10, 13, 14, col. 2, lines 6-51, col. 3, lines 21-55, col. 4, lines 25-66, col. 5, lines 1-5, 29-65, col. 6, lines 50-67.	1-20, 22-25, 28-30, 32-33, 37, 40-41 — 21, 38 — 26-27, 31, 34-36, 39
Y	ASTION et al. The Application of Backpropagation Neural Networks to Problems in Pathology and Laboratory Medicine. Arch Pathol Lab Med. October 1992. Vol 116, pages 995-1001.	1-25, 28-30, 32-33, 37-38, 40

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	X	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier document published on or after the international filing date	Y	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	A	document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means		
"P" document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

26 MAY 2000

Date of mailing of the international search report

13 JUN 2000

Name and mailing address of the ISA/US
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/02987

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	POHL et al. The Quick Machine-A Mathematical Model for the Extrinsic Activation of Coagulation. Haemostasis May 1994. Vol. 24, pages 325-337.	1-25, 28-30, 32-33, 37-38, 40
Y	HOFFMAN et al. THE COAG-A-MATE RA4 FIBRINOGEN ASSAY: A Modification of the Clauss Fibrinogen Method Suitable for Photo-Optical Analyzers. Organon Teknika. 1990, pages 3-7.	3, 6-9, 21, 29-30, 38

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/02987

B. FIELDS SEARCHED

Minimum documentation searched

Classification System: U.S.

702/22, 28, 30, 32, 23, 27, 29, 31, 128, 131, 139, 179, 180, 183, FOR 115 - FOR 119, FOR 170, FOR 171, FOR 131;
703/11, 6, 9, 12; 706/21, 20, 924; 700/266, 268; 73/64.43; 436/66, 43, 47, 48, 49, 50, 54, 55, 69, 174, 164, 171, 180,
805; 422/50, 61, 62, 63, 64, 65, 66, 67, 68.1, 73, 82.05; 382/133, 134, 156, 157, 158, 159; 356/39, 40, 42; 435/13;
377/10, 11